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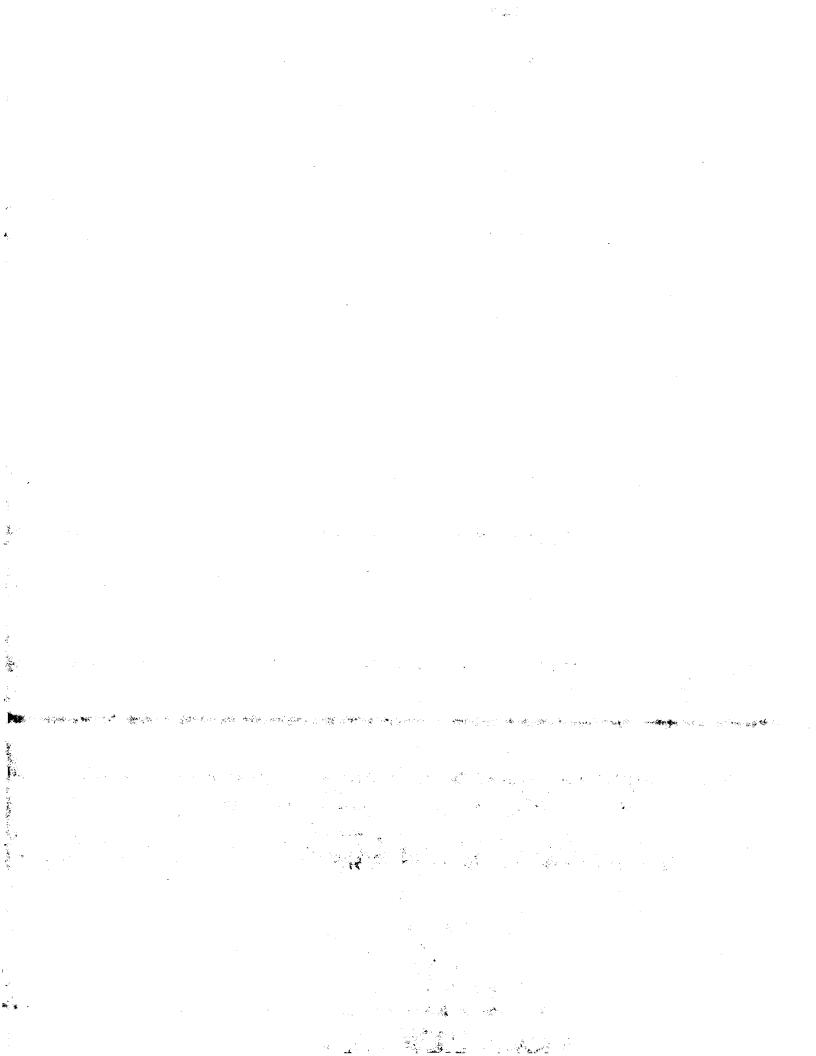
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Sequence 1, Appl1
Sequence 1, Appl1
Sequence 16, Appl
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Sequence 11, Appl
Sequence 21, Appl
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Sequence 24, Appl
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/ cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/NCS06_PUBM_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US06_PUBM_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-99-423A-14

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US-09-792-356-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             870385 seqs, 699768693 residues
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Listing first 45 summaries
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Sequence 15, Appl
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Sequence 19, Appl
Sequence 3, Appli
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Sequence 236, Appli
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               Sequence 7, A
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            US-09-899-429A-7
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LOCATION: (1) .. (1368)
NAME/KEY: 819_Peptide
LOCATION: (1) .. (87)
NAME/KEY: misc_feature
LOCATION: (88) .. (120)
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo saplens
SOFTWARE: Pater
SEQ ID NO 1
LENGTH: 1368
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                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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LOCATION: (88)...(120)
OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by OTHER INFORMATION: extracellular proteases following secretion. NAME/KEY: misc_feature LOCATION: (606)..(633)
OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by

1140

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GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCCTTCAGAAG 1020
                               GCCGTGGTGGAGAACGTGCCCCCGTTGCGTTGGAAGGAATTCGTGCGGCGCCTAGGGCTG
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APPLICANT: Hauptmann: Radolph
APPLICANT: Hampler, Adolph
APPLICANT: Hamler, Adolph
APPLICANT: Hamler, Adolph
APPLICANT: Hamler, Adolph
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAS
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
FILE REFERENCE: 98-38-3
CURRENT APPLICATION NUMBER: US/09/899,429A
CURRENT APPLICATION NUMBER: 09/792,356
PRIOR PELING DATE: 1200-02-23
PRIOR PELING DATE: 1955-06-07
PRIOR PELING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/133,676
PRIOR APPLICATION NUMBER: 08/13,287
PRIOR PILING DATE: 1993-11-17
PRIOR PILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PATENTING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 97
SEQ ID NO 1
FEATURE OF SEC ID NOS: 97
FEATURE TARGET OF NOS: 97
FEATURE OF SEC ID NOS: 97
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CTHER INFORMATION: portion of TNF-BP pro protein cleaved by OTHER INFORMATION: extracellular proteases following secretion NAME/KEX: misc_feature
CCATION: (606)..(633)
CTHER INFORMATION: portion of TNF-BP pro protein cleaved by OTHER INFORMATION: extracellular proteases following secretion US-09-899-429A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09899429A; Patent No. US20020169118A1; GENERAL INFORMATION:
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LOCATION: (1)..(1365)
NAME/KEY: s1g_peptide
LOCATION: (1)..(87)
NAME/KEY: misc_feature
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; OTHER INFORMATION: extracellular proteases following secretion US-09-898-234-1
                                             Length
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                                          100.0%; Score 1368;
100.0%; Pred. No. 0;
iive 0; Mismatches
                                            Query Match 100.
Best Local Similarity 100.
Matches 1368; Conservative
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Coding

us-09-899-422a-1.rnpb

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Query Match 100.0%; Score 1368; DB 9; Length 1368; Best Local Similarity 100.0%; Pred. No. 0;) Indels 0; Gaps 0; Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy Indels 0; Gaps 0; 0; Qy 61 GGANTATACCCTCACGGGCTATTGGACTGCTCCACCTAGGGGACAGGAGAGAG 120 Qy 61 GGANTATACCCTCAGGGGTATTGGACTGGTCCTCACCTAGGGGACAGGGAGAGGA 120 Qy 61 GGANTATACCCCTCAGGGGTATTGGACTGGTCCTCACCTAGGGGACAGGAGAGA 120 Qy 61 GGANTATACCCCTCAGGGTTATTGGACTGGTCCTCACCTAGGGGACAGGAGAGA 120 Qy 121 GATAGTGGTCTCCCCAGGGAAATTATTCCACCTCACACTAGATATTGCTGTACC 180 Qy 121 GATAGTGTGTCCCCAAGGAAATTATTGACATGACTCCAGGCCGGGGAGGATACGGAC 240 Qy 181 AAGTGCCACAAAGGAAATTGTACAATGACTGCCAGGCCGGGCAGGAGATACGGAC 240 Qy 191 111111111111111111111111111111111111	- 연구인 제구제 인구인 원구원 제구제 원구원 원구원 인구인 원구분 원구분 인구인 인구	Db 961 GCTGACCCTTGCGACAGCCTCGCCTCGACCCCATCCCCAACCCCTTCAGAAG 1020

Qy 1081 GCCGTGGTGGAGAACGTGCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTG 1140 Db 1081 GCCGTGGTGGAGAACGTGCCCCGGTTGCGCAAGGAATTCGTGCGCGCCTAGGGCTG 1140 Db 1141 AGCGACCACGAGATCGATGCGCTGCAGAACGGGCGTGCGCGCGC	RESULT 4 US-09-899-422-1 Sequence 1, Application US/09899422 Patent No. US2002009676a1 GENERAL INFORMATION: APPLICANT: Hamber, Radolph APPLICANT: Hammler, Adolph APPLICANT: Hammler, Adolph APPLICANT: Maurer-Fogy, Inggid APPLICANT: Statcwa, Christian TITLE OF INVENTION: Them TITLE OF INVENTION: The Receptors, TNF Binding Proteins and DNAS Coding for TITLE OF INVENTION: Them TITLE OF INVENTION: Them PINER REFERENCE: 98,385-H CURRENT FILING DATE: 2001-08-21 PRIOR FILING DATE: 2000-03-15 PRIOR FILING DATE: 1995-01-17 PRIOR PELING DATE: 1993-11-17 PRIOR FILING DATE: 1993-11-17 PRIOR FILING DATE: 1993-11-17 PRIOR FILING DATE: 1992-01-02 PRIOR FILING DATE: 1992-01-02 PRIOR FILING DATE: 1992-01-02 PRIOR FILING DATE: 1992-01-02	PRIOR FILING DATE: 1990-04-20
ATGGGCCTCTCCACCGTGCCTGCTGCTGCTGCTGGTGCTCTGGAGCTGTTGGTG	301 AGCTGCTCCAAATGCGAAAGGAAATGGGTCAGGTGGAGATCTTCTTGCACAGTGGAC 360	661 GGTCTTTGCCTTTTATCCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGGAG 720

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0y 1321 CTTTGCGGCCCGGCCTCCGCCGGGCCCAGTCTTCTCAGATGA 1368 	ESULT 6 S-09-89 Sequen Patent GENERA APPLI	Ma St NVEN	; FILE REFERENCE: 98-385-J ; CURRENT APPLICATION NUMBER: US/09/899,429A ; CURRENT FILING DATE: 2001-07-03 ; PRIOR APPLICATION NUMBER: 09/792,356	FRIOR FILING DATE: 1000-02-23 PRIOR PELING DATE: 1955-06-07 PRIOR FILING DATE: 1955-06-07 PRIOR PPPLICATION NUMBER: 09/383,676	FRIOR FILING DATE: 1993-02-01 PRIOR PELLING DATE: 1993-11-17 PRIOR FILING DATE: 07/821,750	FRIOK FILING DATE: 1992-01-02; PRIOR APPLICATION NUMBER: 07/511,430; PRIOR FILING DATE: 1990-04-20; NUMBER OF SEQ ID NOS: 97	ស្ត			Ouery Match 100.0%; Score 1368; DB 9; Length 2141; Best Local Similarity 100.0%; Pred. No. 0; Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG 60 11 1 1 1 1 1 1 1 1 1 1 1	QY 61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGAGAAGAGA 120	QY 121 GATAGTGTGTCCCCAAGGAAAATATATCCACCTCAAAATAATTCGATTTGCTGTTACC 180	OY 181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGGCAGGATACGGAC 240	QY 241 TGCAGGGAGTGTGAGAGCGGCTCCTTCACGGTTCAGAAAACCACTCAGACACTGCCTC 300	QY 301 AGCTGCTCCAAATGCCGAAAGGAAATGGCTCGCTGGAGATCTCTTCTTGCACAGTGGAC 360	Qy 361 CGGGACACCGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAAACCTT 420
241 TGCAGGGAGTGTGAGAGCGCCTCCTCACGCTTCAGAAACCACCTCAGACACTGCCTC 300	301 AGCTGCTCCAAATGCCGAAAGGACAATGGGTCGGGGGTCTCTTGTGCAGTGGAC 360	421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGGG 480	481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTC	541 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 600 	601 AATGTTAAGGGCACTGAGGACTCAGGCACACAGTGCTGTTGCTGGTCATTTTCTTT 660 	661 GGTCTTTGCTTTTATCCCTCTCTTCATTGGTTTAATGTATCGCTACCAAGGGTGGAAG 720 	721 TCCAAGCTCTACTCCATTGTTTGTGGAAATCGACACCTGAAAAGGGGGGGG	781 GGAACTACTAAGCCCCTGGCCCCAAACCTTCAGTCCCATCCAGGCTTCACC 840 	841 CCCACCTGGGCTTCAGTCCCGTGCCCACTTCACCTCCAGCTCCAGCTATACC 900	901 CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGGTGGCACCACACCCTATCAGGGG 960 	GCTGACCCCATCCTTGCGACAGCCTCGCCTCCGACCCCATCCCCAACCCCTTCAGAGGGGGCCCCATCCCCAACCCTTCAGAGGGGGGGG	CTGTAC 	366CTG 366CTG	SCGCAA 11111		CTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATCGAGGGCGCGCTGCTGGAGGACATCGAGGACGTGCTTGGGGCTGCTTGGAGGACATCGAGGACGTGCTTGCT	0.000 to 1.000 to 1.0

**RPELICANT: Hauptmann, Rudolph APPLICANT: Himmler, Adolph APPLICANT: Himmler, Adolph APPLICANT: Hauptmann, Christian TITLE OF INVENTION: Them TITLE OF INVENTION: Them FILE REFERENCE: 98,385-6 CURRENT APPLICATION NUMBER: US/09/792,356 CURRENT FILING DATE: 1995-06-07 PRIOR APPLICATION NUMBER: 08/477,639 PRIOR APPLICATION NUMBER: 08/33,676 PRIOR APPLICATION NUMBER: 08/383,676 PRIOR APPLICATION NUMBER: 08/33,287 PRIOR APPLICATION NUMBER: 08/33,287	PRIOR FILING DATE: 1993-11-17 PRIOR APPLICATION NUMBER: 07/821, PRIOR FILING DATE: 1992-01-02 PRIOR APPLICATION NUMBER: 07/511, PRIOR FILING DATE: 1990-04-20 NUMBER OF SEQ ID NOS: 87 SOFTWARE: PATENTIN VET. 2.0	1	Overy Match Query Match Query Match Query Matches 1368; DB 9; Length 2141; Best Local Similarity 100.0%; Pred. No. 0; Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy	Qy 61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGAGAAGAA 120	QY 181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGGGGCAGGATACGGAC 240 DD 393 AAGTGCCACAAAGGAACCTTGTACAATGACTGTCCAGGCCGGGGCAGGATACGGAC 452 QY 241 TGCAGGGAGTGTGAAGCTCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300 DD 453 TGCAGGGAGTGTGAAGAGCGCTCCTTCACCGCTTCAGAAAACCACTCAGACACTGCCTC 310 A53 TGCAGGGAGTGTGAAGAGCGCTCCTTCACCGCTTCAGAAAACCACTCAGACACTGCCTC 512	OY 301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTTTTTGCACAGTGGAC 360	421 TTCCAGTGCTTCAATTGCAGCCTCTGCTCAATGGGACCGTCCTCTCTGCCAGGAG 421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCCATGGGACCGTCCACCTCTCTGCCAGGAG 633 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCCTGCCAGGAG 631 AACAGAACACCGTGCACCTGCCATGCAGGTTTCTTTCTAAGAAAACGAGTGTGTC 693 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTC
	601 AATGTTAAGGGCACTGAGGACCACAGTGCTGTTGCCCCTGGTCATTTCTTT 660	TCCAAGCTCTACTCCATTGTGGGAAATCGACACCTGAAAAGAGGGGGAGCTTGAA	CCCACCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTCCACCTCCAGCTCCACCTATACC [GCTGACCCCTTCTGCGCCTCGGCCTCCGACCCCCACCCCCTTCAGAGG GCTGACCCCATCCCTTCAGAGGC GCTGACCCCATCCCTGCGCTTCGCGACCCCTTCAGAGG GCTGACCCCATCCCTGCGCTTCGCGACCCCTTCAGAGG TGGGAGGCCACAGCCCTCGCCTCCGACCCCTTCCCCTTCAGAGG TGGGAGGACAGCCCCACAGCCCACAGGCCTCCCCAACCCCTTCAGAGG TGGGAGGACAGCCCACAAGCCCACAGGCCTACACTGATGCCCCGGACGCTGTAC TGGGAGGACACAGCCCCACAAGCCCACAGAGCCTTAGATGTCTCCCCGCGACGCTGTAC TGGGAGGACACACCCACAAGCCCACAGAGCCTTAGATGTTTTTTTT			1321 CTTTGCGCCCCCCCCCCCCCCCCCCCCCCCCCCAGAGA 1368

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TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACAACTTCAGACACTTCAGAAAACACTTCAGAGAGCGCTCCTTCACCGCTTCAGAAAACCACCTCAGAGAGCGGCTCCTTCACGCTTCAGAAAACCACCTCAGAAAACCTCAGAGAGCGCCTC
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                                                                                                                                                               ; LOCATION: (213)...(1580)
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R; OTHER INFORMATION: 1TNF-R2
US-09-899-422-16
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                                                                                                                                                                                                                           Length
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1368; Conservative 0; Mismatches
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 16
LENGTH: 2141
TYPE: DNA
CORANISM: Artificial Sequence
                                                                                                                                                        NAME/KEY: CDS
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Patent No. US20020090676A1
GENERAL INFORMATION:
APPLICANT: Hummler, Adolph
APPLICANT: Hummler, Adolph
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
CURRENT APPLICATION WUMBER: US/09/899,422
CURRENT APPLICATION NUMBER: 09/525,998
PRIOR APPLICATION NUMBER: 09/525,998
PRIOR PILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 08/383,676
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                                                                                                                     TCCAAGCTCTACTCCATTGTGGGAAATCGACACCTGAAAAGAGGGGGAGCTTGAA 780
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GCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTG
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APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in J
FILE REFERENCE: 4421-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/21,379
PRIOR APPLICATION NUMBER: US 60/21,379
PRIOR FILING DATE: 2000-10-02
FRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
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No. 0;
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GCCTAGGGCTG 11	Db 1507 CTTGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CONTESTED STATEMENTS: ADDRESSEE: BADRAISS: CITY: Washington STATE: D.C. COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: Patement PC-DOS/MS-DOS SOFTWARE: Patement Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/120,397	FILING DATE: 12 Apr-2002 CLASSIFICATION: CURKNOWN> PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: US/08/054,970 FILING DATE: 03-MAY-1993 ATTORNEY/AGENT INFORMATION: NAME: TOWNSEND, Kevin G. REGISTRATION NUMBER: WALLACH-9 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPAX: 202-628-5197 TELEX: 248633 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2175 base pairs	TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE: NAME/KEY: CDS LOCATION: 256.1620 SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-120-397-1 Query Match Best Local Similarity 99.9%; Score 1366.4; DB 12; Length 2175;

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61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGAGAAGAA 120	TGCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC	301 AGCTGCTCCAAATGCCGAAAGGAATGGGTCAGGTGGAGATCTCTTTTGCACAGTGGAC 360 361 CGGGACACCGTGTGTGGCTGCAGGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420 111111111111111111111111111111111111			781 GGAACTACTACTACTCCCTGGCCCCAAGCTTCAGTCCCACTCCAGGCTTCACC 840 841 CCCACCCTGGGCTTCAGTCCGGTGCCCAGTTCACCTCCAGTCCCACTCCAGCTTCACC 840 111111111111111111111111111111111111	GCTGACCCCATCCTTGCGACACCCTCGCCTCGACCCCATCCCCACCCCTTCAGAAG 	
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Qy 1081 GCCGTGGTGGAAACGTGCCCCGTTGCAAGGAATTCGTGCGCGCCTAGGGCTG 1140 Db 1336 GCCGTGGTGCGCCCCGTTGCGCTGAAGGAATTCGTGCGGCGCCTAGGGCTG 1395 Qy 1141 AGCGACCACGAACCTGCCCCGCAGGCTGCAAGGAACGGCGCGCGC		RESULT 11 US-10-252-408-3 ; Sequence 3, Application US/10252408 ; Publication No. US20030082736A1 ; GENERAL INFORMATION: ; TILE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS ; FILE REFERENCE: A-71592	CURRENT APPLICATION NUMBER: US/10/252,408 CURRENT FILING DATE: 2002-09-24 PRIOR APPLICATION NUMBER: US/08/406,824 PRIOR FILING DATE: 1995-03-20 FRIOR APPLICATION NUMBER: US 08/255,849 PRIOR FILING DATE: 1994-06-08 PRIOR APPLICATION NUMBER: US 07/860,710 PRIOR APPLICATION NUMBER: US 07/860,710 PRIOR APPLICATION NUMBER: US 07/523,635 PRIOR APPLICATION NUMBER: US 07/523,635	PRIOR APPLICATION NUMBER: US 07/421,417 PRIOR FILING DATE: 1989-10-13 PRIOR PILING DATE: 1989-10-13 PRIOR FILING DATE: 1989-09-11 PRIOR FILING DATE: 1989-09-05 NUMBER OF SEQ ID NOS: 29 SOFTWARE: Patentin version 3.1 SEQ ID NO 3 LENGTH: 1368 TYPE: DAA	CONSTANT HOMO Saplens FEATURE: NAME/KEY: CDS LOCATION: (1)(1365) FEATURE: NAME/KEY: mat.peptide LOCATION: (121)() COTION: (121)()	alg_peptide (1)(120) BMATION:	Ouery Match Query Match Best Local Similarity 99.8%; Pred. No. 0; Matches 1365; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 ATGGGCTCTCCACCGTGCCTGCTGCTGCTGCTGCTGTGTGTG

Qy 241 TGCAGGGATGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACTGCCTC 300 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	481 AACAGAACCCTGTGCACTGCATGCAGTTTCTTTCTAAGAAAACGATGTGTC 541 TCCTGTAGTAACACTGTGCACTGCAGTGTTCTTTCTTAAGAAAACGAGTGTGTC 542 TCCTGTAGTAACTGTAAGAAAAGCCTGAGTGAGTGTTCTTTCT	RESULT 13 US-09-792-356-11 US-09-792-356-11 Sequence 11, Application US/09792356 ; Publication No. US20020183485A1 ; GENERAL INFORMATION: ; APPLICANT: Hampler, Adolph ; APPLICANT: Hampler, Adolph ; APPLICANT: Maurer-Fogy, Ingrid ; APPLICANT: Stratowa, Christian ; TITLE OF INVENTION: Them ; TITLE OF INVENTION: Them
0y 1141 AGCGACCACGAGATCGGCTGGAGCTGCAGAACGGGCGCTGCTGCCGGGAGCGCAA 1200 1141 AGCGACCACGAGATCGGTCGAGCTGCAGACGGCGCTGCTGCCTGC	Sequence 11, Application US/09898234 APPLICANT: Hampler, Adolph APPLICANT: Hampler, Adolph APPLICANT: Hampler, Adolph APPLICANT: Stratowa, Christian TITLE OF INVENTION: TWR Receptors, TNF Binding Proteins and DNAS Coding TITLE OF INVENTION: TWR Receptors, TNF Binding Proteins and DNAS Coding TITLE OF INVENTION: TWR Receptors, TNF Binding Proteins and DNAS Coding TITLE OF INVENTION: TWR Receptors, TNF Binding Proteins and DNAS Coding TITLE OF INVENTION: TWR Receptors, TNF Binding Proteins and DNAS Coding TITLE OF INVENTION: TWR Receptors, TNF Binding Proteins and DNAS Coding TITLE OF INVENTION: TWR Receptors, TNF Binding Proteins and DNAS Coding TITLE OF INVENTION: TWR Receptors, 109/25, 998 PRIOR FILING DATE: 109/20-01 PRIOR FILING DATE: 1992-02-01 PRIOR FILING DATE: 1992-01-02 PRIOR PILING DATE: 1992-01-02 PRIOR FILING DATE: 1992-04-10 PRIOR PILING DATE: 1990-04-20 SOFTWARE: PAREIT OF 1990-04-20 NUMBER OF SED ID NOS: 80 SOFTWARE: PAREIT OF 1990-04-20 LEGOTH: 1334 ORGANISM: ATLIFICIAL Sequence FRAVIER: TROUMATION: LambdaTNF-BPI5 and PTNF-BPI5 vectors LOCATION: (213)(1325) COTHER INFORMATION: LambdaTNF-BPI5 and PTNF-BPI5 vectors OTHER INFORMATION: LambdaTNF-BPI5 and PTNF-BPI5 of Indels 0; Gaps 1 ATGGGCCTCCACCCGCCCCCCCCCCCCCCCCCCCCCCCC	Oy 61 GGAATATACCCTCAGGGGTTATTGGACTGGTCCCTCAGGGGACAGGGACAGGGACAGGG

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APPLICANT: Himmler, Adolph
APPLICANT: Maruer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
APPLICANT: Stratowa, Christian
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TITLE OF INVENTION: Them
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CURRENT APPLICATION NUMBER: US/09/899,422

CURRENT FILICN DATE: 2001-08-21

PRIOR APPLICATION NUMBER: 09/525,998

PRIOR FILING DATE: 1995-00.01

PRIOR FILING DATE: 1995-00.01

PRIOR PILING DATE: 1995-00.01

PRIOR FILING DATE: 1995-01.02

PRIOR FILING DATE: 1993-11-17

PRIOR FILING DATE: 1993-11-17

PRIOR FILING DATE: 1992-01-02

PRIOR FILING DATE: 1990-04-20

SEQ ID NO 11

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LENGRH: 1334
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Patent No. US20020090676A1
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OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: LambdaTNF-BP15 and pTNF-BP15 vectors
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FILE REFERENCE: 98,385-G
CURRENT APPLICATION NUMBER: US/09/792,356
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 08/407,639
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR PLICATION NUMBER: 08/153,287
PRIOR PLICATION NUMBER: 07/821,750
PRIOR PLICATION NUMBER: 07/821,750
PRIOR PLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1993-01-02
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1900-04-20
                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (21)
                                                                                                                                                                                                                                                                                   LENGTH: 1334
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for

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Sequence 21, Application US/0989429A

Patent No. US20020169118A1

GENERAL INRORMATION:

APPLICANT: Hauptmann, Rudolph
APPLICANT: Hammler, Adolph
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: Them
FILE REFERENCE: 98-385-J
CURRENT APPLICATION NUMBER: US/09/899,429A
CURRENT FILING DATE: 2000-02-23
FRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1992-01-0781/30
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 97
SEQ ID NO 21
FROM THE PATENT OF THE PATE
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81.7%; Score 1117.2;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1119; Conservative 0; Mismatches
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; LOCATION: (213)..(1325)
US-09-899-429A-21
                                                                                                  US-09-899-429A-21
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1 CGGGACACCGTGTGGCTGCAGGAACCAGTACCGGCATTATTGGAGTGAAACCTT	1 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCATGGGACCGTGCACCTCTCCTGCCAGGAG	1 AAACAGAACACGTGTGCACCTGCCATGCAGGTTTCTTTCT	1 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCCTACCCCAGATTGAG	1 AAIGHTAAGGGCACTGAGGACTCAGGCACACAGTGCTGTTGCTCTGGTCATTTTCTTT	1 GGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGGAAG	1 TCCAAGCTGTACTCCATTGTTTGTGGGAAATCGACACTGAAAAGAGGGGGGGG	1 GGAACTACTACTAAGCCCTGGCCCCAAACCTACAGGTTCAGTCCCACTCCAGGCTTCACC	1 CCCACCCTGGGCTTCAGTCCCGTGCCCAGCTTCCACCTTCACCTCCAGCTCCACCTATACC	1 CCCGGFGACTGTCCCAACTTTGCGGCTCCCCGCAGAGGTGGCACCCCCTATCAGGGGIIIIIIIIII	1 GCTGACCCCATCCTTGCGACAGCCCTCGACCCCCATCCCCAACCCCCTTCAGAAG 	1 TGGGAGGACGGCCCACAAGCCACAGAGCCTAGACACTGATGACCCGGGGGGCGTGTAC	1 GCCGTGGTGGAGAACGTGCCCCGTTGCGCTGGAAGAATTC 1122 	
361 573	421	481	541 753	601	661	721	781 993	841 1053	901	961 1173	1021	1081	
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Search completed: June 9, 2003, 01:17:52 Job time: 214 secs

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Appli Appli Appli Appl

> Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Seq

Sequence Sequence Sequence

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APPLICANT: Brenda F. Baker and Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF THERI
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            US-08-050-3118-56
US-08-050-3118-56
US-08-804-166-34
US-08-804-166-3
US-08-910-991-3
US-08-910-991-1
                            US-08-050-319B-47
US-08-465-982-47
US-08-941-166-7
US-08-910-991-7
US-08-910-991-5
US-09-149-922-6
US-08-050-319B-1
US-08-050-319B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Isis Pharmaceuticals, Inc. STREET: 2292 Faraday Avenue CITY: Carlsbad COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,038A
FILING DATE: June 26, 1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Laurel Spear Bernstein
REGISTRATION NUMBER: 37,280
REFERENCE/DOCKET NUMBER: RTS-0004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (760) 931-9200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
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   Command line parameters:
-MODEL-frame+_p2n.model -DEV-x1p
-O-/cgn2_1/G577_14726/app_query.fasta_1.647
-O-/cgn2_1/USPTO_spool/US0989422/runat_04062003_145737_14726/app_query.fasta_1.647
-O-/cgn2_1/USPTO_spool/US09899422/runat_04062003_145737_14726/app_query.fasta_1.647
-DB-1ssued_Patents_NA -QFWT-fastap -SUFFIX=n1 -MINMATGH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-b1ts -START-1 -END--1 -MATRIX=blosum62 -TRANS-human40.cd1
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-USBE-LOCAL -OUTFWT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USBE-LOSAB99422_cCN 1.1_61_erunat_04062003_14577_14726 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NGG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_INMEOUT-120 -WARN_TIMENOUT-30 -THREADS-1 -XGAPOP=10 -XGAPEXT-0.5 -FGAPOP=6
-FGAPEXT-7 -YGAPOP=10 -YGAPEXT-0.5 -DELOP=6 -DELEXT-7
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11: /cgn2_6/ptodatcal/ina/5A_COMB.seq:*
12: /cgn2_6/ptodatcal/ina/5B_COMB.seq:*
13: /cgn2_6/ptodatcal/ina/6A_COMB.seq:*
14: /cgn2_6/ptodatcal/ina/6B_COMB.seq:*
15: /cgn2_6/ptodatcal/ina/PCTUS_COMB.seq:*
16: /cgn2_6/ptodatcal/ina/PcTUS_COMB.seq:*
16: /cgn2_6/ptodatcal/ina/PcTUS_COMB.seq:*
16: /cgn2_6/ptodatcal/ina/PcTUS_COMB.seq:*
16: /cgn2_6/ptodatcal/ina/PcTUS_COMB.seq:*
16: /cgn2_6/ptodatcal/ina/PcCTUS_COMB.seq:*
16: /cgn2_6/ptodat
                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                              - nucleic search, using frame_plus_p2n model
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US-09-505-250-3
US-08-321-668-1
US-08-126-016-1
US-08-126-016-1
US-08-050-319B-24
US-08-465-982-24
US-08-762-308-10
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US-08-286-740-2
PCT-US95-09576-2
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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            ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly
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Patent No. 6329148
Patent No. 6329148
GENERAL INFORMATION:
APPLICANT: Rosen, Glenn
TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
TITLE OF INVENTION: Triptolides and Death Domain Ligands
FILE REFERENCE: SUN-109PRV2
CURRENT APPLICATION NUMBER: US/09/505,250A
CURRENT FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2161
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Matches:
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Best Local Similarity:
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LOCATION: (25)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                            3.09e-229
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; STRANDEDNESS: sir; TOPOLOGY: linear US-09-106-038A-1
                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                     Alignment Scores:
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401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu
          GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: BRAKEBOUSCH, Cord
APPLICANT: JAFFOLOMEEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE THE RECEPTORS, THEIR PREPARATION AND THEIR INUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NATA:
FILING DAPE: 12-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
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Matches:
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TELECOMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
                                                                                                                                         Sequence 1, Application US/08321668
Patent No. 5665859
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
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STRANDEDNESS: single
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                                                                                        CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
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                                                LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp
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321 AlaaspProlleLeuAlaThrAlaLeuAlaSerAspProlleProAsnProLeuGlnLys	1336 GCCGTGGTGGAGAACGTGCCCCGTTGCGAAGGAATTCGTGGGCGCCTAGGGCTG 139 381 SerAspHisGlulleAspArgLeuGluLeuGluAsnGlyArgCysLeuArgGluAlaGlu 400	DD 1395 AUCGACGACGACGACGACGACGACGACGACGGCGCTGCCGCGAGGGCGCAA 1455 QY 401 TyrSerMetLeualaThrTrpArgArgArgThrProArgArgGlualaThrLeuGluLeu 420	421 LeuGlyArgvalLeuArgAspMetAspLeuGlyCysLeuGluAspIleGluGluAla 440	Db 1576 CTTTGCGGCCCGCGCCCGCGCCCGCGCCCAGTCTTCTCAGA 1620 RESULT 5 US-08-126-016-1 ; Sequence 1, Application US/08126016	; FACUL NO. 3011201; ; GENERAL INFORMATION: ; APPLICANT: WALLACH, DAVID ; APPLICANT: NOPHAR, YARON ; APPLICANT: KEMPER, OLIVER	IUT ION OF THE RECOMBINANT TUMO	** 🖼 🌭	STREET: 419 Seventh Street, N.W., Suite 300 ; CITY: Washington ; STATE: DC ; COUNTRY: USA	COMPUTER REAL REDIUM TYPI COMPUTER:	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.25 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/126,016	. d	FILING DATE: 13-DEC-1990 ; ATTORNEY/AGENTINFORMATION: ; NAME: BROWDY, ROGER L ; REGISTRATION NUMBER: 25,618	T	INFORMATION FOR SEG ID NO: 1: SEQUENCE CHARACTERISTICS: LENGIH: 2175 base pairs TYPE: nucleic acid
Pred. No.: 3.12e-229 Length: 2175 Score: 2487.00 Matches: 455 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 B8: 1 Gaps: 0 US-09-829-422A-2 (1-455) x US-08-837-941-1 (1-2175)	Oy 1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeuLeuVal 20	Db 316 GGAATATACCCTCAGGGGTATTGGACTGGTCCTCACCTAGGGGACAGGGAAGAGAGA 375 Qy 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnAsnSerIleCysCysTyr 60 111111111111111111111111111111111111	LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 	4 ∺ 1/	121 ArgaspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu	Oy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160	Oy 161 LysGinAsnThrValcysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180	Oy 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIlleGlu 200	Qy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220	Oy 221 GlyLeuCysLeuLeuSerLeuLeuPhelleGlyLeuMetTyrArgTyrGlnArgTrpLys 240	Oy 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260	Oy · 261 GlyThrThrThrLySProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280	Qy 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr 300 	Oy 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320

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                                                         GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr
                                             ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr
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APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
TITLE OF INFURION:
NUMBER OF SEQUENCES: 8
CORRESPEDUBENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STREET: 0.C.
CONTEXT: USA
ZIP: 20004
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MEDIUM TYPE: Floppy disk
COMPUTER: Elappy disk
COMPUTER: Elap Rc Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/054,970
FILING DATE: 03-MAX-1993
CLASSIFICATION: 435
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Patent No. 6395267
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NAME: TOWNSEND, KET 34, 033
REFERENCE/DOCKET NUMBER: WALL.
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
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TELEFAX: 248633
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Mismatches:
Indels:
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Matches:
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2487,00
100,00%
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                                                                      ; NAME_KEY: mat_peptide
; LOCATION: 319..1620
US-08-126-016-1
                                        NAME/KEY: CDS
LOCATION: 256..1620
FEATURE:
                    MOLECULE TYPE: CDNA
          linear
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Best Local Similarity:
Query Match:
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                  1216 GCTGACCCCATCCTTGCGACAGCCCTCGACCCCATCCCCAACCCCTTCAGAAG
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Patent No. 5633145

GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                        3.12e-229
2487.00
100.00%
100.00%
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                        NAME/KEY: CDS
LOCATION: 256..1620
                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                             Alignment Scores:
                                                                                                                                   US-08-054-970-1
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APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBRR OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94301
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Matches:
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Mismatches:
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TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
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2482.00
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99.78%
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Best Local Similarity:
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Patent No. 592548
GENERAL INFORMATION:
APPLICANT: Beatler, Bruce A.
APPLICANT: Bazzoni, Flavia M.
TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
TITLE OF INVENTION: SIGNAL
NUMBER OF SEQUENCES: 11
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & ISTREET: P.O. Box 4433
CITY: Houston
STATE: TX
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COMPUTER READABLE FORM:
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Mismatches:
Indels:
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Matches:
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2062 base pairs
TYPE: nucleic acid
STRANBURES: double
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2482.00
99.78%
99.78%
                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                    NAME/KEY: CDS
LOCATION: 155..1519
US-08-465-982-24
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Best Local Similarity:
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Pred. No.:
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                                 756 CTAGGTCTTTGCCTTCTATCCTTTATCTTCAGTTTAATGTGCCGATATCCCCGGTGG
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                                                                                                                                                                                                                                                                                                                                                335 ProAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGlnSerLeuAspThrAsp
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                                                                                               260 GluGlyThrThrLysProLeu-----AlaProAsnProSerPheSerProThrPro
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APPLICANT: Taylor, J. Michael
APPLICANT: Taylor, J., Marcus
APPLICANT: Taylor, J., Marcus
APPLICANT: Lee, Eun-Kyung
APPLICANT: Mangi, Simon
TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 08411-018001
CURRENT APPLICATION NUMBER: US/09/513,007
CURRENT APPLICATION NUMBER: US/09/513,007
CURRENT FILING DATE: 1999-02-25
PRIOR FILING DATE: 1999-02-26
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2440
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; LOCATION: (294)...(1706)
US-09-513-007-1
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                UTSD: 335--1
APPLICATION NUMBER: US 08/224,593
FILING DATE: 05-APR-1994
ATTORNEY AGENT INFORMATION:
                                         NAME: KITCHELL, BEATBAIR S.
REGISTRATION NUMBER: 33,928
REFRENCE/DOCKET NUMBER: UTSD:
TELECOMMUNICATION: INFORMATION:
TELEPAN: 474-757
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                              1.8e-136
1521.00
75.61%
65.19%
61.16%
                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                   Alignment Scores:
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US-08-762-308-10
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318 TyrGlnGlyAlaAspProlleLeu	Db 1344 ACCCCAGTTCAGAAGTGGGAAGCCCCCCAGCGCCCCCGATCAGCTCGCGGATGCC 1403 Oy 355 AspProAlaThrLeuTyrAlaValValGluAsnValProProLeuArgTrpLysGluPhe 374	1404 395 1524 415 1584	Qy 435 GluaspIleGluGluAlaLeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeu 454 :::	GENERAL INFORMATION: APPLICANT: CTOWLEY, CTAIG W. TITLE OF INVENTION: HEATHOD FOR SELECTING HIGH-EXPRESSING TITLE OF INVENTION: HOST CELLS TITLE OF INVENTION: HOST CELLS TOWNERS OF SEQUENCES: ADDRESSEE: Genentech, Inc. STREET: 460 Point San Bruno Blvd CTOWNERS OUTH San Francisco STATE: California COURTY: SOUTH SAN FRANCISCO TOWNERS OF STATE: CALIFORNIA	A PARTICION OF THE PART	ATTORNEY/AGENT INFORMATION: NAME: Lee, Wendy M. REGISTRATION NUMBER: 798 FELECOMMUNICATION INFORMATION: TELEPAN: 415/25-1994 TELEPAN: 415/95-9881 TELEPAN: 415/95-9881 TELERY: 910/31-7168 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 6889 bases TYPE: nucleic acid
Alignment Scores: 6.23e-136	Db 294 ATGGCCTCCCCACCGGCCTGCCTGCTGCTGCTGCTGTTGCA 353 Qy 21 GlylleTyrProSerGlyValileGlyLeuValProHisLeuGlyAspArgGluLysArg 40 ::: :: :	414 GAGAGTCCCTGTCCCCAGGAAATATAACCCGCGAAAATAGCACCTTTGCTGCACCCGCAAAATAGCACCCCGCAAAATAGCACCCCCCAAAATAGCACCCCCCCAAAATAGCACCCCCCCC	DD 534 TGCAGGGTGTGTGCCCTGGCACCTTGGAGAACCATCTCAGACGATGCCTG 593 QY	0y 141 PheGInCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160 1	0y 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProleuVall1ePhePhe	261 GlyThrThrLysProLeualaProAsnProSerPheSerProThrProGlyPheThr 1071

; STRANDEDNESS: double ; TOPOLOGY: linear US-08-286-740-2	Qy 296 SerSerThrTyrThrProGlyAspCysProAsnPhealaAlaProArgArgGluVal 314
Ard Jonnent Scores: 5.27e-107 Length: 6889 Pred. No.: 1223.50 Matches: 257 Score: 64.04% Conservative: 19 Percent Similarity: 59.63% Mismatches: 61 Query Match: 1 Gaps: 11 DB: 1 Gaps: 11	315 Al 2412 CC 334 eP
-422A-2 (1-455) x US-08-286-740-2 (1-6889)	2434CAGCACCTGAACTCCTGGGAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
1 MetGlyLeuSerThrValProAspLeuLeuLeuValCeuValLeuLeuGluLeuLeuVal 20 	Qy 351LeuAspThrAspAspProAlaThrLeuTyrAlaValValGluAsnVal 366
21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40 [Oy 367ProProLeuargTrpLysGluPheValargArgLeuGlyLeuSerAspH1sGl 384
41 AspSerValCysProGlnGlyLysTyrileHisProGlnAsnAsnSerileCysCysThr 60	Qy 384 ulleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGlnTyrSerMe 403 :: ::: ::
61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnaspThrasp 80 	Qy 403 tLeu-AlaThrTrpArgArgArgThrPro 412
81 CysargGluCysGluSerGlySerPheThralaSerGluAsnHisLeuargHisCysLeu 100 	~ 5.5
101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120 	; APPLICANT: GENENTECH, INC. ; TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING ; TITLE OF INVENTION: HOST CELLS ; NUMBER OF SEQUENCES: 4
121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140 	复货 62
141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160 	STATE: California COUNTRY: USA LIP: 94.080 COMPUTER READABLE FORM:
161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180 	; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk ; COMPUTER: ISM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: patin (Genentech)
181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200 	CURRENT APPLICATION DATA: ; APPLICATION NUMBER: PCT/US95/09576 ; FILING DATE: ; CLASSIFICATION:
i 20 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220 {}}	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 08/286740 ; FILING DATE: 05-AUG-1994 ; ATTORNEY/AGENT THOORMATION:
<pre>GlyLeuCysLeuLeuSerLeuLeuPhelleGlyLeuMetTyrArgTyrGlnArgTrpLys</pre>	. 🤇
237 2237 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeu 259	TELECOMOUNICATION TELECOMOUNICATION: TELECOMOUNICATION TELEPHONE: 415/225-1994 TELEFAX: 415/952-988
≨	; INFORMATION FOR SEQ 10 NO: 2:
260GluGlyThrThrTysProLeualaProAsnProSerPheSerPro 275 :::	SEQUENCE CHARATERISTICS: LENGTH: 6889 bases TYPE: nucleic acid STRANDEDNESS: double
276 ThrProGlyPheThrProThrLeuGlyPheSerProValProSerSerThrPheThrSer 295	ine

Oy 315 AlaProPro-TyrGlnGlyAlaAspProlleLeuAlaThrAlaLeuAlaSerAspProll 334	Db 2434CAGCACCTGAACTCCTGGGAGGACGTCAGTTTCCTCTCCCCCTALATION 2489 Qy 351 LeuaspThraspAspProalaThrLeuTyralaValQuasnVal 366	Qy 367ProProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisGl 384	Qy 384 ulleaspargLeuGluLeuGlnAsnGlyArgCysLeuArgGlualaGlnTyrSerMe 403	RESULT 13 US-08-627-151A-6 ; Sequence 6, Application US/08627151A ; Patent No. 5866341	LILA,	SC 13	ចិត្ត 🖺	COUNTRY: USA ZIP: 92121 COMPUTER READABLE FORM: MEDIOW TYPE: Diskette	COMPUTER: IBM Compatible ; OPERATING SYSTEM: DOS ; SOFTWARE: FastSED for Windows Version 2.0 ; CURRENT APPLICATION DATA:	; APPLICATION NUMBER: US/08/627,151A ; FILING DATE: 03-APR-1996 ; CLASSIFICATION: 435 ; PRIOR APPLICATION DATA:	FILING DATE: ATTORNEY/AGENT INFORMATION: ATTORNEY FICHER CATION	REGISTRATION NUMBER: 36,510 REFERENCE/DOCKET NUMBER: CBIO16 TELECOMMUNICATION INFORMATION: TELEPHONE: 619-410-8926	TELERA: 619-410-8928 ; TELEA: ; INFORMATION FOR SEQ ID NO: 6: ; SEQUENCE CHARACTERISTICS:	; TENGTH: 6896 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear	US-08-627-151A-6 Alignment Scores: 5.62e-104 Length: 6896 Score: 1192.00 Matches: 211
Pred. No.: 5.27e-107 Length: 6889 Score: 1223.50 Matches: 257 Percent Similarity: 64.04% Conservative: 19 Best Local Similarity: 59.63% Mismatches: 61 Query Match: 49.20% Indels: 95 Query Match: 5 6308: 11	09-899-422A-2 (1-455) x PCT-US95-09576-2 (1-6889) 1 MetGlyLeuSerThrValProAspLeuLeuLeuValLeuLeuCluLeuLeuVal	DD 1609 AIGGGCCTCTCCACCGTGCCTGCTGCTGCTGCTGGTGGTGGTGGTGGTGGTGG	41 AspservalcysprogladilylystyrileHisproglamanashserileCysCysThr	Qy 81 CysargGluCysGluSerGlySerPheThralaSerGluAsnH1sLeuArgH1sCysLeu 100	Oy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120	Qy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140 	Qy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160	Qy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180	Qy 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGln11eGlu 200	Oy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220	Oy 221 GlyLeuCysLeuLeuSerLeuLeuPhelleGlyLeuMetTyrArgTyrGlnArgTrpLys 240	241 SerLysLeuTyrSerlleValCysGlyLysSerThrProGluLysGluGlyGluLeu 2238GACAAGAGTTGAGATTCAAA	Qy 260GluGlyThrThrThrLysProLeuAlaProAsnProSerPheSerPro 275 ::	Qy 276 ThrProGlyPheThrProThrLeuGlyPheSerProValProSerSerThrPheThrSer 295 Db 111111 2319 ACACCT	Qy 296 SerSerThrTyrThrProGlyAspCysProAsnPheAlaAlaProArgArgCluVal 314

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                                                                         1295 CGGGACACCGTGTGTGGCTGCAGGAACAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
                                                                                                                                                                                                                                                                                                                                                                                        PheGlnCysPheAsnCysSerLeuCysLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu
                                                                                                                                                                                                             LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp
                                                                                                                                                                                                                                                        CyaArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu
                                                                                                                                                                                                                                                                                                                                             121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.JC. Turner, F.W. Brennan
TITLE OF INVERTION: Modified human TWEalpha (Tumor
TITLE OF INVERTION: NETONICES:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
COMPUTRY: USA
ZIP: 94301
COMPUTRY: USA
ZIP: 94301
COMPUTER: FLOPPY disk
COMPUTER: INM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, version #1.25
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Conservative:
Mismatches:
Indels:
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                                  Gaps:
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47.93%
Percent Similarity:
Best Local Similarity:
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US:08-050-319B-47
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SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIle 199
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                            Indels:
     APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISCHATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 31,550-0030
TELECOMMUNICATION INFORMATION:
TELEPRAM: (415) 327-3231
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                              3.87e-99
1124.00
99.508
99.508
45.208
CURRENT APPLICATION DATA:
                                                                                                                                                                                    MOLECULE TYPE: CDNA to
                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-050-319B-47
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Pred. No.:
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AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
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198
0
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                       Sequence 47, Application US/08465982
Patent No. 5863786
GENERAL INFORMATION:
APPLICANT: M.F.Eldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.W Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
SORTWARE APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
FILING DATE:
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            ZIP: 94.901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                      3: Reed & Robbins
635 Bryant Street
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CITY: Palo Alto
STATE: California
COUNTRY: USA
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MOLECULE TYPE:
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US-08-465-982-47
RESULT 15
US-08-465-982-47
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CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu
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AF32997 Rattus no AF329978 Rattus no AF329978 Rattus no AF32998 Rattus no AF32998 Rattus no M59377 Murine tumo M60468 Mouse_tumor K59238 Murine mRNA BC004599 Mus muscul

X57796 Mouse mRNA

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M75866 Human tumor

AC006057 Homo sapi AF329976 Rattus no AX401925 Sequence M63122 Rat tumor n

A29103 H.saplens m AB051103 Felis cat U19994 Sus scrofa AX131997 Homo sapi

164751 Sequence 1 A19907 Synthette n BC010140 Homo sapi 143805 Sequence 24 AK056611 Homo sapi A20255 55kD recept M60275 Human tumor

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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-Q-/cgn2_1/USPTO_spool/US0999422/runat_04062003_145736_14704/app_query.fasta_1.647
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-UNITS-blts -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
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-USDEN-USREGUGERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOR-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DBLOP-6 -DELEXT-7
                                                                                                    June 9, 2003, 00:13:39; Search time 2999 Seconds (without alignments) 4415.397 Million cell updates/sec
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1 MGLSTVPDLLLPLVLLELLV......DIEBALCGPAALPPAPSLLR 455
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                         OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                2054640 seqs, 14551402878 residues
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Maximum Match 100%
Listing first 45 summaries
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Database :

M33294 Human tumor A26412 cDNA for (5 AX409713 Sequence M58286 Homo sapien

A29098 Synthetic D A21522 TNF alpha g

Description

M63121 Human tumor AR096330 Sequence X55313 H.sapiens T A43873 Sequence 1

A43873 Sequence 1 A78738 Sequence 7 AR041076 Sequence

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Location/Qualifiers
1. 2062
//Organism="Homo sapiens"
//db_arref="taxon:9606"
155. 1522
                                         601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT
             361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu
                                                                                                                                                                                                                                 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr
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/db_xref="GI:579600"
/db_xref="SWISS-PROT:P19438"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic construct.

synthetic construct
artificial sequences.

1 (bases 1 to 1368)
Hauptmann, R., Himmler, A., Maurer-Fogy, I. and Stratowa, C.
Pubracett: EP 0393438-A 48 24-0CT-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H
      DNA linear From patent EP0393438.
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Matches:
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    1368
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/translation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
GOKKIHPONDSICCTKCHKGTYLYNDCPGPGODTCRECESGSFTASENHLRHGLSG
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PNPLQKWEDSAHKPQSLDTDDPATLYAVPROMPPLAWREFYRRLGLSDHEIDRLELCN
GRCLREAQYSMLATWRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPA
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Matches:
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HUMTNPR
HUMAN tumor necrosis factor receptor mRNA, complete cds.

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Gell:339744
Gell:339744
Gell surface receptor; tumor necrosis factor receptor.
Human placenta, cDNA to mRNA.
ISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.

TE (passa 1 to 2087)
Schall, T.J., Lewis, M., Koller, K.J., Lee, A.L., Rice, G.C., Wong, G.H., Gatanaga, T., Granger, G.A., Lentz, R., Raab, H., Kohr, W.J. and
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Location/Qualifiers

1. .2087

/organism="Homo sapiens"
/db_xref="taxon:9606"
182. .1549
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FFGLCLLSLLFTGLAFFRYRYRKKSKLYSIVCGKSTPEREGELECTTTRFLAPRYSFSPT
PGFTPTLGFSPVPSSTFTSSSTYTFGDCPNFAAPRREVAPFYGGADFILATALASDPI
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ORS Brockhaus, M., Dembic, Z., Gentz, R., Lesslauer, W., Loetscher, H. and LE Ture-binding proteins
RNAL Patent: EP 0417563-A 2 4 20-MAR-1991;
F. HOFFMANN-LA ROCHE AG
ORES 1. catlon/Qualifiers
Source //Organism="synthetic construct"
// Ab.rref="taxon:32630"
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Gene expression profiles in liver cancer
Patent: WO 0229103-A 2360 11-APR-2002;
GENE LOGIC INC (US)
Location/Qualifiers
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                                                421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla
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M58286.1 G1:339753
Lumor necrosis factor receptor.
Human cell line HL60, cDNA to mRNA.
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/gene="TNF receptor"
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                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Pfizenmaler, A., Maurer-Fogy, I., Kronke, M., Scheurich, P., Pfizenmaler, K., Lantz, M., Olsson, I., Hauptmann, R., Stratowa, C. and Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein

DNA Cell Biol. 9 (10), 705-715 (1990)
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             AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2161)
Nophary: Kemper,O., Brakebusch,C., Englemann,H., Zwang,R.,
Aderka,D., Holtmann,H. and Wallach,D.
Solubbe forms of tumor necrosis factor receptors (TNF-Rs). The of the type I TNF-R, cloned using amino acid sequence data of soluble form, encodes both the cell surface and a soluble form of
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REFERENCE 1 (bases 1 to 2175) AUTHORS Wallach, D., Nophar, Y., Kemper, O., Engelmann, H., Brakebusch, C. and Adarka, D. TITLE Expression of the recombinant tumor necrosis factor binding protein I (TBP-1) JOURNAL Patent: US 5311261-A 1 22-SEP-1998; FEATURES Location/Qualifiers Source //organism="unknown" BASE COUNT 474 a 641 c 604 g 456 t	Alignment Scores: 2.99e-154 Length: 2175 Score: 2.897.00 Matches: 455 Score: 2.897.00 Matches: 455 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0 Gs-99-422A-2 (1-455) x ARO41076 (1-2175)	Oy 1 MetGlyLeuSerThrValProAspLeuLeuLeuPolLeuLeuGluLeuLeuVal 20	QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60	Qy 81 CysArgGluCysGluSerGlySerPherhrAlaSerGluAsnBisLeuArgHisCysLeu 100 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140	Qy 161 LysGlnAsnThrValCysThrCysHisalaGlyPhePheLeuArgGluAsnGluCysVal 180	Qy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValllePhePhe 220
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1 MetGlyLeuSerThrValProAspLeuLeuLeuValLeuLeuGluLeuLeuVal 20	LyscysHisLysclyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnaspThrasp 80 LyscysHisLysclyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnaspThrasp 80 AGTGCCAAAGGAACTACTT[SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValasp 12	141 PROGREGATION SPECIAL LANGUAGE AND TRANSMILLS ENDOSTRONGE 150 676 TICCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACGTGCACCTCCTGCCAGGAG 735 161 LysGlnAsnThrValCysThrCysHisalaGlyPhePheLeuArgGluAsnGluCysVal 180 161 LysGlnAsnThrValCysThrCysHisalaGlyPhePheLeuArgGluAsnGluCysVal 180 161 [111111111111111111111111111111111		241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260	281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300	321 AlaAspProfleLeuAlaThrAlaLeuAlaSerAspProfleProAsnProLeuGlnLys 340
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101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120		22 91 24 97	241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260	ProfhrieudlyPheserProValProSerSerThrPheThrSerSerThrTyrThr 	340 127 360 133	361 AlavalvalGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380	401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420 11111111111111111111111111111111111	Oy 441 LeucysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
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336 GCCGTGGTGCAGAGCCCCCGTTGCCGTGGAAGGAATTCGTCCGGCGCCTAGGGCTG 381 SerAspHisGluileAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 111111111111111111111111111111111111	1516 441 1576	RESULT 14 A19907 A19907 AA19907 ACCESSION A19907 ACCESSION A19907 ACCESSION A19907 ASTRICTION A19907 AND AND A19907 ASTRICTION A19907 AST	E C C C C C C C C C C C C C C C C C C C	YEDA	Alignment Scores: 2 99e-154 Length: 2176 Score: 2487.00 Matches: 455 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 DB: 6 Gaps: 0 UGS-09-899-422A-2 (1-455) x A19907 (1-2176)	1 MetGlyLeuSerThrvalProAspLeuLeuLeuProLeuValLeuLeuGluLeuLeuVal 20 1	AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr	81 CysargGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 10

Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 9	-09-899-422A-2 (1-455) x BC010140 (1-2194)	1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGluLeuVal 	241 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG	Qy 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40	Oy 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60	61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp	Db 421 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGATATGGAC 480	Qy 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100		Db 541 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCGGTGGGTGG	Qy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140	141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 16	Db 661 TTCCAGIGCTTCAATTGCAGCCTCTGCCTCAATGGGACGTGCACGTGCTCTCTGCCAGGAG 720	Oy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180	181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 2		Qy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValllePhePhe 220	DD 901 GGTCTTTGCCTTTTATCCCTCCTCTTCATGGTTTAATGTATCGCTACCAACGGTGGAAG 960	Qy 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260	991 ICCARACICIACICCATIGITGIGGGGAAAICGACAC 261 GlyfhrfhriwsProleuAlaProAsnProSerP	1021 GGAACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCACTCAGGCTTCACC 10	Qy 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr 300		Db 1141 CCCGGGGGCTCCCAACTTTGCGGCTCCCCGCAGAGAGGGGCACCACCTATCAGGGG 1200	Qy 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
BC010140 LOCUS BC010140 DEFINITION Homo saptens, tumor necrosis factor receptor superfamily, member 1A, clone MGc:19588 IMAGE:411360, mRNA, complete cds.	z	sapiens. sapiens	Euk Man	1 (bases 1 to 2194) Strausberg, R. Direct Submission	JOURNAL Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov COMMENT Contact: mGC help desk	Enert: Cydpus: remain.hin.gov. Tissue Procurement: ATC: CDNA Library Preparation: Rubin Laboratory	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),	Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc mqc@nhgri.nih.gov		Dietrich, N.L., Guan, X., Gupta, J., Ho, SL., Karlins, E., Legaspi, R., Lim, H., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantribop, S., Thomas, P.J.	Tiongson, E. E., Touchman, J. W., Tsurgeon, C., Vogt, J. L., Walker, M.A., Zhang, L H. and Green, E. D.	Clone distribution: MGC clone distribution information can be found	CHICOGOI THE INTEGER. 27 ROW: IN COLUMN: ALT. HILLS://linage.lini.gov Series: IRAL Plate: 27 Row: In Column: 25 This clone was selected for full length sequencing because it nasced the following selection critical matched mpNa di. 33975		/organism="Homo sapiens" //db_wref="Locusin:7132" //db_wref="town.orof="town.	/clone_11958 IMAGE:4131360" /tlssue_type="Muscle, rhabdomyosarcoma" /clone_11b="NIH_MGC_17"	CDS 4411508 /codon_start=1 /product=#!mor necrosis factor recentor ennerfamily	member 1A member 1A / Protein id= Ash10140.1"	/translation="MGLSTYPPLILPLVVLELLVGIYPSGVIGLVPHGDREKRDSVC PQGXYIHPQNNSICCTKCHKGTYLYNCPGPGODTDCRECESGSFTASENHLRHCLSC	SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE KQNTVCTGAGFFRENECSCSNCKKSLEGFTKLCLPQIEBVWGTSDSGTTVLLELVU FIGUR FOR FOR FOR FOR FOR FOR FOR FOR FOR FO	FFOLCHISHER OLDS IT REGENERATE STYCORS THE ROBE LEGIT IT RELARBISES FT PER STYLED FOR ST	BASE COUNT 478 a 644 c 600 g 472 t	ORIGIN A) tenmont conso.	Allynment Scores: 3.02e-154 Length: 2194 Pred. No.: 2487.00 Matches: 455

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1076)

NIH-MGC.http://mqc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbarfemali.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The Th.M.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

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High quality sequence stop: 727.

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BM923204.1 GI:19373583
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BM923204 AGENCOURT
BQ723672 AGENCOURT
AL559050 AL559050
BIB60918 603390284
AU117362 AU117362
AU131978 AU131978
                                                                                                                  June 8, 2003, 20:48:38; Search time 1864 Seconds (without alignments) 11885.958 Million cell updates/sec
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                                                                                                                                                                                                                             1 atgggcctctccaccgtgcc.....cgcccagtcttctcagatga 1368
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                                                                                                                                                                                                                                                                                                                                                         32308132
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                     16154066 seqs, 8097743376 residues
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Maximum Match 100%
Listing first 45 summaries
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AL559050
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Maximum DB seq length: 200000000
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source

FEATURES

809.8 803.6 764.6 703.6 689

Score

Š. Result

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BQ723672
AGENCOURT_8489850 Lupski_dorsal_root_ganglion Homo saplens cDNA clone IMAGE:6184295 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'-TCGACCCAGCGTCCG-3' and 5'-TCGACCCCACCGTCG-3'. Size selected > 5'-GACTAGTTCTAGATCGCGAGCGCCGCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capps=rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone through the I.M.A.G.E. Consortium/LLNL at:
http://magge.llnl.gov
Plate: LLAM13573 row: d column: 24
High quality sequence stop: 607.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV-SPORT6 (Life Technologies); Sit NotI: Site_2: SalI; cDNA made by oligo-dr priming. Directionally cloned using the following adaptors:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
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//organism="Homo sapiens"
//db_ref="Faxon:9606"
//clone="IMAGE:6184295"
//clone=lib="Lupski_dorsal_root_ganglion"
                                       /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
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283 c
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                                                                                            /note=*Organ: pooled colon, kidney, stomach; Vector:
pCNV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (ECORV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1:3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library.*
6 others
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                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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Pred. No. 2.1e-189;
0; Mismatches 5; Indels 0;
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5758757"
                                                        /clone_lib="NIH_MGC_116"
/lab_host="DH10B"
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Best Local Similarity 99.4%;
Matches 811; Conservative
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FEATURES	BASE COUNT ORIGIN Query Match Best Local Matches 77 QY 193	5 8 8 8 8 8 8 8 8	3 6, 8 6 8 6 8 6	8 6 8 6 8 6
Qy 291 ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCGGGTGGGGTCGGTGGGGTCCTTCTTG 350 181 ACACTGCCTCAGCTGCTCCAAATGCCGAAAGGGAAATGGGTCGGTGGAGATCTCTTCTTG 240 351 CACAGTGGACCGGTGCTGCAGGAAGGAACTGGTGCGGCATTATTGGAG 410 241 CACAGTGGACCGGGACCCGTGTGTGGCTGCAGGAACAGTACCGGCATTATTGGAG 300 411 TGAAAACTTTTCCAGTGTGTGGCTTGCAGGAAGAACCAGTACCGGCATTATTGGAG 300 Qy 411 TGAAAACTTTTCCAGTGCTTCAATTGCAGCCTCTCCCTCAATGGGACCGTGCACCTCTC 470 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		DD ACGGREGAAGTCCAAGGTCTACTCCATTGTTGGGGAAATCGACCTGAAAAGAGGG 60 ACGGREGAAGGTCCAACTCTACTACTCCATTGTTTGTGGGAAATCGACACTGAAAAGAGGG 60 771 GGGGCTTGAAGGACTACTACTACTACGGCCCCAAACCCCAAGCTTCAGTCCCACTCC 830 11111111111111111111111111111111111	841 CACCCCTATCAGGGGGGCTG 1006 AACCCCC 1012 901 CATTCC 907 0 AL559050 ION AL559050 ION AL559050 NAL559050 NAL559050 NAL559050 NAL559050	KEYMORDS EST. SOURCE human. ORGANISM Homo sapiens ENTERENCE TO STATE TO STATE THE STATE TO STATE TO STATE THE STATE TO STATE TO STATE TO STATE THE STATE TO STATE TO STATE THE STATE TO STATE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 889)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1538-53-3975
Fax: 81-438-52-3975
Fax: 81-438-52-3996
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
HRI human cDNA project; 5'- & 4 Gressarch Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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/tissue_type="whole embryo, mainly head"
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301 c 249 g 166 t 6 other:
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/db_xref="taxon:9606"
/clone="HEMBA1001229"
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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// Organism-"Homo sapiens"
// Organism-"Homo sapiens"
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// Clone-lib-"NIH_MGC_87"
// Clone-lib-"NIH_MGC_87"
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// Issue_type-"mammary adenocarcinom
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Euthoria: Euthoria; Primates; Catarrhini; Hominidae; Bomo.
Euthoria: Euthoria; Primates; Catarrhini; Hominidae; Bomo.
Is NIH-MGC http://mgc.nci.nih.gov/.
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: EutDrDrp
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC Clone distribution information can be http://mage.llnl.gov
Plate: LLAM12017 row: h column: 21
High quality sequence stop: 740.
                                                                                                                                                         60330284F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5399108 5', BI860918
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/cell_line="NT2"
/note="Vector: pweeks retinoic acid (RA) induction"
a 199 c 201 g 179 t 4 others
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3966
Exai: genomics@hri.co.jp
Exail: genomics@hri.co.jp
Exail: genomics@hri.co.jp
Rix human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                     62 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGCTCCTGGAGCTGTTGGTG
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                                                                                                                      Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 3;
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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/lab_host="DH10B"
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BM546826
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/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="DH10B"
/notc="Organ: brain; Vector: pCMVSPORT 6; ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies. Contact is Feng Liang Life Technologies. Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filangelifetech.com URL: http://fullength.invitrogen.com" 3 others
                              AL529836 LII_NFL001_NBC4 Homo sapiens cDNA clone CS0DD005YP05 5
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                                                                                                                                            Homo sapiens

Wararyota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 942)

1 (bases 1 to 942)

1 (Aruber.C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization

Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="csobbo05yp05"
/clone_lih="LTI_NFL001_NBC4"
/sex="male"
                                                                                           AL529836.1 GI:12793329
                                                              mRNA sequence.
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ISM Hounon sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CE 1 (bases 1 to 1070)
RS NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/
Email: gapba: Temail.nih.gov
Tissue Procurement: Invitrogen
CONTACT: Robert Strausberg, Ph.D.
Email: gapba: Temail.nih.gov
Tissue Procurement: Invitrogen
CONTA Library Preparation: Life Technologies, Inc.
CONTA Library Preparation: Life Technologies, Inc.
CONTA Library Arrayed by: The I.M.A.G.E. Consortium
CONTA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MgC colone distribution information can be http://image.lin.gov
Plate: LLAM12711 row: g column: 14
High quality sequence start: 2
High quality sequence start: 2
High quality sequence stop: 669.

EES I.M.A.G.E. Consortium/Library Location/Qualifiers
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AGENCOURT_6491128 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723557
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Pred. No. 2.8e-157;
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GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAG
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                                              : www.genoscope.cns.fr
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Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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Pred. No. 6.9e-157;
4; Mismatches 8;
                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.
Location/Qualifiers
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Best Local Similarity 97.9%;
Matches 704; Conservative
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
38;
Mismatches
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AL577008 LTI_NFL006_PL2 Homo :
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BG180101 974 bp mRNA linear EST 06-FEB-2001 602329676F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431019 5', mRNA sequence.
BG180101 GI:12686804
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 974)
                                                928 CCCCGCAGAGAGGTGGCACCACCTATCAGGGGGCTGACCCCATCCTTGCGACAGCCCTC
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1 (Dases 1 to 669)

8 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

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Email: yongsungémal. Kribb.re.kr

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Site_2: NotI: The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including ECOR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about GOT. The CDNA vector was
circularized with E. coli DNA ligase after digestion of
ECORI which site is also included in vector. An RNA strand
converted to a DNA strand by Oksyama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli ToplOF' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
                                                                                                                                                                                                            BM742388 669 bp mRNA linear EST 01-MAR-2002 K-EST0015556 S6SNU620 Homo sapiens cDNA clone S6SNU620-5-C12 5', mRNA sequence.
BM742388.1 GI:19063703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                 688 ATTGGTTTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTGTGGG
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100.0%; Pred. No. 1.2e-154;
ative 0; Mismatches 0; Indels
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/cell_type="Sattering floating"
/cell_line="sNU-620"
/lab_host="ToplOF'"
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/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="S6SNU620-5-C12"
/clone=11b="S6SNU620"
/sex="F"
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High quality sequence stop: 669.
Location/Qualifiers
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900

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Note-Organ: Lung, Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I: Site_2: Not I: Not_CGAP_DIO is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oilgo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into PT73-Pac vector. The oilgonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the sequence that is located between the Not I site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        838 ACCCCACCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGGTCCACCTT 897
                                                                                                                                                                                                                                                                                                                                                                                                of IOWR
                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 696)
                                                                                                                                                                                                                                                                                                 Contact: Robert Straubberg, Ph.D.
Bmall: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/Libri at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
Sequence: 669-696, >GC_rich#Low_complexity
FOUNA-YES.
                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unbublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             658 ITTGGTCTTTGCCTTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGG
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IMAGE:5862208 3', mRNA sequence.
BM989994
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/organism="homo sapiens"
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/clone=lib="NCLCGAP_DIO"
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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/db_xref="taxon:9606"
/clone="IMAGE:4431019"
/clone=lib=NHLMGC=1"
/tissue_type="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma, cell line"
/tab_host="bullob (phage=resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NH_MGC Library."
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                                                                                                                                                                                                                                                                                      Length 974;
                                                                                                                                                                                                                                                                                      Score 668.6; DB 12; Length
Pred. No. 1.6e-154;
0; Mismatches 34; Indels
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al Similarity 95.3%;
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994 bp mRNA linear EST 05-MAR-2002
AGENCOUR_6415909 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531041
5', mRNA sequence.
BM800044
                                                                                                                                                                                                       Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Ammanla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 994)
                                                                                                                                                                                                                                                 654 ITTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTAATGTATCGCTACCAACG
                                                                                                                                                                                                                                                                                                                              1 TITCITIGGICITITGCCITITATCCCTCCTCTTCATTGGITTAATGIATCGCTACCAACG
                                                                                                                                                                                       GTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGAGGGGGA
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                Gaps
    a NCI_CGAP Library."
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                                                              Score 667; DB 12;
Pred. No. 3.8e-154;
0; Mismatches 10;
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                                                             tch 48.8%;
al Similarity 98.4%;
684; Conservative
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                                                                Query Match
                                                                              Best Local
Matches 68
                   BASE COUNT
ORIGIN
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JOURNAL
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BM800044
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602626965F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4751536 5',
                                957
                                                                                                        102 GGGGTGACCCCATCCTTGCGACCCTCGCCTCCGACCCCATCCCCAACCCCTTCAG 361
                                                                                                                                                                                     421
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ACCCCCACCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTAT 241
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone="IMAGB:4751536"
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/tissue_type="squamous cell carcinome"
/lab_host="DH10B (Tl phage-resistant)"
/note="Corgan: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 718)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLANlOGS row: b column: 17
High quality sequence stop: 679.
                            ACCCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGGGTGGCACCCCTATCAG
                                                                                                                                                                                                                                                                                                                                         GGGGCTGACCCCATCCTTGCGACAGCCCTCGGCCTCCGACCCCATCCCCAACCCCCTTCAG
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TITLE
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COMMENT
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BG680679
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1133

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FEATURES

1013

360

300

us-09-899-422a-1.rst

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Contact: Genoscope

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Location/Qualifiers

1. .837

/Organism="Homo sapiens"
/Ab_xref="taxon:9606"
/Alone="Crosson:9606"
/Alone="Crosson:9606"
/Alone="Crosson:Princh"
/Alab_host="DH108"
/Alab_host="DH108"
/Alab_host="DH108"
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/Alab_host="DH108"
/Alab_host="DH109"
/Alab_host
                                                                                                                                                                                                                               AL522989

AL522989 I.TL_NFL004_NBC2 Homo sapiens cDNA clone CSODB009YP14 5
prime, mRNA sequence.
AL522989.1 GI:12786482
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        658 TTTGGTCTTTGCCTTTTATCCCTCTTTTAT---GGTTTAATGTATCGCTACC---AA 711
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                               826 ITTGGGCTTGCCCTTTTATCCCTCCCCTCCATTGGGTTTAAATGGATCGCTACCCCACG
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
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Best Local Similarity 99.8
Matches 639; Conservative
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JOURNAL
COMMENT
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AL522989
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AUTHORS
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/lab_host="DH10B (phage=resistant)"
/note="Gorgan: uterus; vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.1 kb. 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
    Tissue Procurement: Arci
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Preparation: MG.E. Consortium (LLNL)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MG.C. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLAM12212 row: b column: 02
    High quality sequence stop: 654.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGACACCGTGTGTGCCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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47.3%; Score 647.2; DB 14;
Best Local Similarity 94.7%; Pred. No. 3.2e-149;
Matches 713; Conservative 0; Mismatches 31;
                                                                                                                                                                                                                                                 1. :994
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/db_xref="taxon:9606"
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Search completed: June 9, 2003, 00:13:31 Job time : 1870 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

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Run on:

June 8, 2003, 23:42:19; Search time 299 Seconds
(without alignments)
3426.954 Million cell updates/sec
Title:
US-09-899-422A-2
Sequence:
1 MGLSTVPDLILPLVILELLV......DIEEALGGPAALPPAPSLLR 455
Scoring table:
BLOSUM62
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 10.0 , Fgapext 0.5
Egapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

4370478

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: //SID52/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1 AAQ49932 ID AAQ49932 standard; CDNA to mRNA; 1368 BP XX AC AAQ49932;

29-APR-1994 (first entry)

Lambda-derived TNF-R cDNA.

Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-IR; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allograft; xenograft; rejection; graft verses host disease; sepsis; inflammation; allergy;

Homo sapiens.

autoimmune dysfunction; ss.

80

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100 300 120 360 140 160 480 180 540

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AlaaspProlleLeuAlaThrAlaLeuAlaSerAspProlleProAsnProLeuGlnLys 340
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                                                                                            121 GATAGTGTGTCCCCAAGGAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC
                                                LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp
                                                           SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The linker may comprise 5-100 amino acids selected from Cly, Asp, Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion protein is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, dispinosis and assays for conditions madiated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causitive diabetes, multiple sclerosis, pulmonarty fibrosis and silicosis, cerebral malarla, allograft and xenograft rejection in graft verses host disease, sepsis, septic shock, inflammation, allergies and
                                                                                                                                                                                                                                                                                                                                                                            necrosis factor
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                                                                                                                                                                                                                                                                                                                                                                                                 in the
                                                                                                                                                                                                                                                                                                      New fusion protein tumour necrosis factor and human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAQ49931-32 encode human tumour necrosis receptor (TNF-R) and the sequences in AAQ49933-34 encode human interleukin-1 receptor (IL-1R). These sequences were used in production of a fusion protein which conformed to one of the
                                                                                                                                                                                                                                                                                                                  useful in therapy, diagnosis and assays of e.g. arthritis, diabetes, cerebral malaria, sepsis, etc
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TWF-R-11nker-TWF-R-11nker-IL-1R
IL-1R-11nker-TWF-R-11nker-TWF-R
TWF-R-11nker-TWF-R
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4.tag b
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7.tag c
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The present invention relates to polymorphic variants of the tumour necrosis factor receptor 1 (TNRR1) gene. The present sequence is the coding sequence of the TNRR1 gene. The sequence of the whole gene is given in AAA95102, AAA95103 and AAA95104. The polymorphisms were identified by amplifying and sequencing regions of the gene. Twelve polymorphis loci were discovered. Of these twelve polymorphisms, four cause a change in the TNRR1 protein. The TNRR1 polymorphisms may be identifying targeting the biological function of TNRR1 as well as for identifying targeting the protein for treatment of disorders related to its abnormal expression or function such as tumours, apoptosis related disorders and bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                          Polynucleotides comprising polymorphic variants of a reference sequence for tumour necrosis factor receptor 1 (TNFR1), useful for studying the blological function of TNFR1 and identifying drugs targeting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeuLeuVal
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                                                                                                                                                                                                                                                 Chew A;
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein for treating disorders
                                                                                             GENAISSANCE PHARM INC.
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23-FEB-2000; 2000WO-US04606.
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                                                                                                                       NANDABALAN K.
SCHULZ V P.
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us-09-899-422a-2.rng

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The sequence is that of DNA encoding tumour necrosis factor alpha binding protein which was obtd. from a human placental cDNA library in lambda gill using a probe (AAQ20974). The DNA also encodes the extracellular domain of human TNF alpha receptor and as such it is useful for treating diseases where TNF alpha is involved as a causative agent, e.g. cachexia, sepsis and autoimmune diseases, specifically rheumatoid arthritis. See also AAQ20974.
                                                                                                                                                                                                     /*tag= e
/note= "encodes the extracellular domain of human
                                            88
                                                                                                                                                                                                                                                                                                                                                                                              New tumour necrosis factor alpha binding protein and polypeptide - useful in treating cachexia, sepsis and auto immune diseases e.g. rheumatoid arthritis
                                         necrosis factor alpha; autoimmune diseases; cachectin;
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242..751
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                                                                                          Cocation/Qualiflers
155..1522
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 25pp; English.
                      TNF-alpha binding protein gene.
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275..1522
/*tag= c
473..532
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155..274
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                                                   extracellular domain.
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P-PSDB; AAR20787.
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AlaAspProlleLeuAlaThrAlaLeuAlaSerAspProlleProAsnProLeuGlnLys
                             PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu
                                                                     LysGlnAsnThrValCysThrCysH1sAlaGlyPhePheLeuArgGluAsnGluCysVal
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1414

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This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA library in gtl0 was screened with probe AAQ29236. Ten hybridising clones were plaque purified and cDNA size determined by PAGE against an Eco RI digested phage DNA. The inserts of two cDNA clones were then sequenced. The coding region of the majority of the human TNF-alpha
New polypeptide capable of binding human TNF alpha - comprises first three cysteine-rich subdomains of TNF alpha receptor for treating autoimmune disease, septic shock, HIV etc.
                                                                                                                                                             tumour necrosis factor alpha; extracellular binding domain;
treatment; pulmonary diseases; septic shock; HIV infection;
malaria; viral meningits; graft versus host disease;
autolimnue disease; rheumatoid arthritis.
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/*tag= e
/codon= Seq:"GAC", aa:Asn
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156..1517
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1258..1260
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                                                                                                                                                Encodes TNF-alpha 55kD receptor.
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P-PSDB; AAR24000.
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AAQ10883 standard; cDNA; 2088
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                                                                                                                                             55kD receptor was isolated as an EcoRI fragment encoding 374 amino acids, and cloned into a mammalian cell expression vector, resulting in prinkr. A derivative of the TNF-alpha receptor was produced by domain. PCR with primaris AAQ29237,8 generated a 300pp restriction fragment which was cloned into prinkr, giving prinkecd. DNA sequencing confirmed this contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected into monkey COS-7 cells.
                                                                                                                                                                     GlylleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg
                                                                                                                                                                                                                      LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp
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                                                                    BP; 429 A; 618 C; 572 G; 443 T; 0 other;
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                                                                                                                                                   GCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTG
                                                                                                                                                                                        30kD INF inhibitor precursor gene in lambda-gt10-7ctnfbp
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                                                      GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr
                                                                                                                                                                                                                                                                                                                                                                                                     TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; IL-1; inflammatory disease; degenerative disease; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 30 kDa TNF inhibitor precursor coding sequence
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18-JUL-1989;
11-DEC-1989;
07-FEB-1990;
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                                                               The sequence encodes the entire 30 kD TNF inhibitor. The clone from which the sequence was obtd. was isolated from a CDNA library prepd. from 937 cells treated with PMA/PHA. The whole gene can be inserted into expression vectors for prepn. of TNF inhibitor for use in the treatment of inflammatory and degenerative
                    suppression of TNF-alpha
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                    our necrosis factor inhibitor - for -beta, useful as therapeutic agent.
                                                Disclosure; Fig 21; 142pp; English
                                                                                                                                           Sequence 2088 BP; 439 A; 626 C;
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AMGEN INC

Ŗ Thompson KK, Brewer MT, Kohno T; Squires C, King MW, Hale K Vanderslice RW, Vannice J,

WPI; 2001-006443/01 P-PSDB; AAB37677.

ģ Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and degenerative diseases mediated

Example 6; Fig 21; 82pp; English.

The present invention relates to Tumour Necrosis Factor (TNF) inhibitors (see AAB37676 and AAB37685), which have TNF inhibitory activity. The novel TNF inhibitors of the present invention are useful as therapeutic for treating inflammatory and degenerative diseases mediated by TNF. The present sequence is the coding sequence for the precursor of 30 kDa TNF inhibitor. The 30 kDa TNF inhibitor can inhibit TNF alpha.

Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;

2088 455 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 2.96e-174 2487.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores:

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SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120 528

140 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160

SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200 181

TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCCACGAAGTTGTGCCTACCCCAGATTGAG 768 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220 828 240 888 1068 948 1128 1129 GCTGACCCATCCTTGCGACAGCCCTCGGCTCCGACCCCATCCCCAACCCCTTCAGAAG 1188 260 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr 300 1488 400 420 440 AlaAspProlleLeualathralaLeualaSerAspProlleProAspProLeuGlnLys necrosis factor binding protein cDNA. Astandard; cDNA; 2111 BP (first entry) Human tumour 201 694 709 18-OCT-1999 301 1069 321 . 1009 1309 AAZ09170 AAZ09170; AAZ09170 ν̈́δ RESULT ò 셤 à 셤 ö g ö đ a λŏ ò g a ò g ò g ç 윱 ò 셤 ò g ö 쉽

Tumour necrosis factor binding protein; TNF; insoluble protein; agonist; auti-inflammatory; antimalarial; treatment; septic shock; inflammation; autoimmune glomerulonephritis; cerebral malaria; immune response; antagonist; diagnosis; ds.

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Location/Qualifiers 187..1554

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                            AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC
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                                                                                                                                                                                                                                                                                                   This invention describes novel homogeneous insoluble proteins (I), their (in)soluble fragments (Ia) and their salts that can bind tumour necrosis factor (TNF). The products of the invention have anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i) to treat diseases in which TNF is involved (e.g. septic shock, autoimmune glomerulonephritis, cerebral malaria, immune responses and inflammation), (Ii) to purify TNF (ant)agonists and (IV) for diagnostic determination of TNF in body fluids. Antibodies raised against (I) are used for affinity purification of (I). This sequence encodes a tumour necrosis factor binding protein described in the method of
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                                                                                                                                                                                                                                                   New insoluble proteins, and fragments, that bind to tumor necrosis factor, used to treat e.g. septic shock or cerebral malaria
                                                                                                                                                                                         Loetscher
                                                                                                                                                                                                                                                                                                                                                                                                                            other;
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        binding
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        TNF.
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89CH-0003319.
90CH-0000746.
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12-SEP-1989;
08-MAR-1990;
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Schlaeger E;
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                                                                                                           31-AUG-1990;
                                       mat_peptide
                                                                  EP939121-A2
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US-09-899-422A-2 (1-455) x AAH48859 (1-2111)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel insoluble proteins (1), also their (in) soluble fragments and pharmaceutically acceptable salts, able to bind tumor necrosis factor (TME) and in homogeneous form. The products of the invention have antiinflammatory, immunosuppressive, antibacterial, to treat diseases mediated by TNF, e.g. shock in cases of meningococcal retact development of autroimmune glomerulonephritis and cerebral malaria. Also (1), or antibodies specific for them, are used for adagnostic determination of TNF in body fluids, for affinity purification of TNF and for identifying (ant) agonists of TNF. This sequence encodes a human TNF binding protein described in the method of the invention.
                                                                                 TNF; tumor necrosis factor binding protein; TNFBP; treatment; insoluble protein; antiinflammatory; immunosuppressive; antibacterial; antiprotozoal; treatment; meningococcal sepsis; cerebral malaria; autoimmune glomerulonephritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                     New homogeneous, insoluble proteins that bind tumor necrosis factor (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
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                                                                                                                                                                                   "TNFBP-associated protein"
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187..1554
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           BP
                                                               Human TNFBP-associated DNA #1
     AAH48859 standard; DNA; 2111
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                                                                                                                                                                                                                                                                                                   89CH-0003319.
90CH-0000746.
90CH-0001347.
90EP-0116707.
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                                              (first entry)
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                                                                                                                                   Homo sapiens
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Schlaeger E;
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Pred. No.:
                         AAH48859;
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Length:
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Mismatches:
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Gaps:

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Percent Similarity; Best Local Similarity; Query Match; DB;

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                                       CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnH1sLeuArgH1sCysLeu
                                                                                     141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu
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        The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the
                                                       400
                                                                                                    401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
                                                                                                                 Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                       SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln
                                                                                                                                                                                                                                                                                                                                                                Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardlac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                           Human cDNA differentially expressed in granulocytic cells #610.
                                                                                                                                                                                                Vockley J;
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                                                                                                                                                                                                                                                                                                                   (first entry)
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gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the minature of inflammation; where the level of expression of the gene is indicative of inflammation; where the level of expression of the gene is indicative of inflammation; where the level of expression of subject, exposure of a subject to a pathogen or sterile inflammation disease, by contacting a tissue having on sterile inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA, M2 is useful for from Gs in the tissue. M1 is useful for detecting an inflammation in a tissue; M4 is useful for detecting an inflammation of especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psporiasis, rheumatoid arthritis, asthma, thrombosis, cardiac reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative collitis, ception injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative collitis, ception injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, crohn's disease, ulcerative collitis, ception of the above conditions. The present sequence atta for this patent did not form part of ormat directly from WIPO at Commat directlon, but was obtained in electronic format directly from WIPO at
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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ANB3563-ANB37455 in a cissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, of markers that can be used to monitor disease states, disease progression, over the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides antisense compounds targeted to human tumour necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds can be used in a method of inhibiting the expression of TNFR1 human cells or tissues. The antisense compounds specifically hybridize with one or acid molecules encoding TNFR1 modulating the function of nucleic acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1 produced. The antisense compounds and method are useful as research reagents and diagnostics, and in the treatment and prophylaxis of infection, inflammation or tumour formation. The present sequence represents the nucleotide sequence of human TNFR1 (Genbank Accn No:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense inhibition of tumor necrosis factor type 1 expression for diagnosis, treatment and prevention of disease, particularly tumors
                                                                            is factor receptor type 1; INFR1; antisense; infection;
tumour formation; INFR1; anticancer; ds.
                                       Human tumour necrosis factor receptor (TNFR1) nucleotide sequence
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Query Match:
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31-MAR-2000
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ABK13194 standard; DNA; 2161

RESULT 13 ABK13194

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This invention relates to a novel method for enhanced killing of tumour cells comprising contacting a tumour cell with a synergistic cells comprising contacting a tumour cell with a synergistic combination of a death domain receptor ligand and a diterpenoid triepoxide. This method has cytostatic activity and works by blocking in the state of the combination may be used for treating tumours, particularly solid tumours, c. invention may be used for treating tumours, particularly solid tumours, also neurological malignancies, particularly solid tumours, also neurological malignancies, non-We cutaneous T-cells, mycosis fungoides, non-We cutaneous T-cells imphoration of papulosis, T-cell rich cutaneous Imphoid hyperplasia, c. lymphomatoid papulosis, T-cell rich cutaneous Imphoid hyperplasia, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered with other active agents, e.g. anti-centered the diterpenoids and the death domain ligands allows increased the testing at equivalent or anti-angiogenic agents. The potent synergy combination and the death domain ligands allows increased resistant cells. This sequence represents the human tumour necrosis factor alpha receptor (TNF-RI) DNA. TNF-RI is a death domain receptor trienancy and the inventor and the papers.
                                                                                                                                                                    diterpenoid trisposide; cytostatic activity; c-IAPJ; c-IAPJ; c-Cardinoms, mammary adenocarcinoms, non-small cell lung carcinoms, neurological malignancy; lichoen planus; non-Bodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic; malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic; non-NF cutaneous T-cell; lymphoma, mycosis fungoides; anti-tumour; T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid; discoid lupus erythematosus; human; gene; receptor; TNF-RI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of a synergistic combination of death domain receptor ligands and diterpenoid triepoxides for killing of tumour cells
                                                                                                                                                        ds; tumour; death domain receptor 11gand;
                                                                                                               Human tumour necrosis factor alpha (TNF alpha) receptor DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha protein"
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99US-149989P.
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                                                                           (first entry)
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P-PSDB; AAU75064.
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20-AUG-1999;
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Length:

Alignment Scores: Pred. No.:

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This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
                                                                                                  New protease capable of cleaving soluble tumour necrosis factor (TNF) receptor - from cell-bound TNF- receptor, useful for
                                                                                                                                                                                                                                                p55; tumour necrosis factor receptor; TNF-R; human; murine; c
epidermal growth factor receptor; EGF-R; protease; inhibitor;
phorbol myristate acetate; PMA; ss.
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/product= p55 TNF-R
2143..2149
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/note= "possible poly-A signal"
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P-PSDB; AAR75084.
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                                                                                                        AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr
                                                                                                                                  LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp
                                                    WetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeuLeuVal
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Matches:
Conservative:
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Indels:
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Expression of this receptor is regulated by shedding of the extracellular receptor fragment. The p55 TNF-R can be shed in response to different inducing agents, e.g. phorbol myrisate acetate (PNA), depending on cell type. The only region of the receptor whose structure affects the shedding response is the spacer region (see AAR75012) in the extracellular domain. This region is located close to a site of cleavage of the molecule, and links the Cys rich module to the transmembrane domain. The spacer region of the encoded protein was used to create the chimeras between human p55 TMF-R and murine epidermal growth factor receptor (EGF-R) that are represented by AAR7507-11. This spacer region vas subjected to deletion mutations (AAR7507-11. This spacer region receptor (EGF-R) that are represented by AAR7507-11. This spacer region was subjected to deletion mutations (AAR75013-25) and substitutions can fade chain identity of these residues, with the exceptor of a limited dependence on the identity of Val 173. Mutations which alter the conformation of the protein adversely effect the shedding process. The mutations shown in AAR75013-47 were introduced in order to create an inhibitor of a protease that is capable of cleaving the soluble TMF-R. This conformation of the cell bound TMF-R. Fragments of these inhibitors can be seen in the inhibitors can be seen in the inhibitors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Encodes human 55kD TNF-binding protein.
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187..273
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                                                                                                                                                                                                                   Partial amino acid sequences were determined for the 55 and 75kD TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were synthesised based on these partial sequences. The primers were used to produce a cDNA fragment for use as aprobe to screen a human placental cDNA bank constructed in lambda gill. Positive clones were identified and sequenced. DNA constructs comprising the TNF-BP coding sequence may also contain a fragment encoding a human Ig domain. Recombinant constructs are used to transform cells to confer limproved TNF-binding properties.
                                                                                                                                                        Insoluble tumour necrosis factor binding proteins - and DNA encoding them, useful in pharmaceutical prods. and for antibody prodn.
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89CH-0003319.
90CH-0000746.
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                                                                                                             Brockhaus M,
Schlaeger EJ;
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12-SEP-1989;
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                                                                                                                                                                                                                                                                                                                                                                        Modification of the tumour necrosis factor receptor by mutation or deletion modulates signal transduction and/or cleavage effected by the receptor. This modulation of activity can also be achieved using effector proteins which interact with the TNF receptor or the effector Molecules which interact with the TNF receptor or the effector proteins can be used to treat or prevent diseases associated with TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft rejection; graft vs. Nost disease or septic shock. They can also be used to treat overdoses of exogenous TNF.
                                                                                                                                                                                                                                                                                                       Modulating activity of tumour necrosis factor receptor - using peptide(s), antibodies, etc. which interact with critical regions of receptor or effector protein, for controlling auto-immune disease, septic shock, etc.
                                                                                                                                  necrosis factor receptor
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                    Tumour necrosis factor receptor coding sequence
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Mismatches:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseg/genesegn-emb1/NA2002.DAT:*

Description	Lambda-derived TNF	Human TNFR1 coding	30kD TNF inhibitor	Human 30 kDa TNF i	Human tumour necro	Human TNFBP-associ	Human cDNA differe	Gene #2360 used to	Human tumour necro
SUMMARIES		AAA95105	AAQ10883	AAC83946	AAZ09170	AAH48859	ABK84039	ABN95862	AAZ48475
B0	14	21	12	22	20	22	24	24	71
å Query e Match Length DB	1368	1368	2088	2088	2111	2111	2111	2111	2161
& Query Match	66.66	6.66	6.66	6.66	6.66	6.66	6.66	6.66	99.8
Score	1366.4	1366.4	1366.4	1366.4	1366.4	1366.4	1366.4	1366.4	1366.4
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12	364	٠.	2175	16	AAQ90513	p55 TNF-R gene. H
. 13	363	ά.	2062	13	AAQ20973	TNF-alpha binding
14	363	ď	2062	13	AAQ24440	Encodes TNF-alpha
15	363	9	2176	17	AA012215	Type I TNF recepto
16	_	σ.	2141	11	AA006285	Human Tumour Necro
17	13	σ.	2170	14	AA050870	p55 Tumour necrosi
18	\circ		1334	11	AA006282	Plasmid Tumour Nec
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21	\sim	w.	6926	18	AAV04431	- 1.1
22	632.4	Ġ	6889	17	AAT15931	DHFR/intron (WTras
23	٠.	'n.	608	13	AA024441	Encodes truncated
24	'n	7	1478	20	AAX58150	CadC-fusion polype
25	-	7	1301	18	AAT94022	CDNA for TBP(20-19
26	0	۲.	1147	18	AAT94021	CDNA for TBP(20-19
27		Ġ.	504	13	AAQ24445	Encodes truncated
28	æ	'n	483	19	AAV41548	Human soluble tumo
29	483	ď.	483	13	AAV19801	. Soluble tumour nec
30	æ	'n.	483	50	AAV81732	Tumour necrosis in
31		35,3	483	22	AAC83945	Human 30 kDa TNF i
32	440	ď	2254	21	AAA95104	Partial human TNFR
33	٠	ä	1049	18	AAT94007	CDNA for TBP(20-16
34	24.	ä	1202	18	AAT94008	
35	н	ö	1674	21	AAZ50196	MalE fusion plasmi
36	38	7	1977	7	ABA99913	
37	76.	7.	477	13	AAQ24444	Encodes truncated
38	75.	ζ.	207	77		Target canine gene
39	57.	œ.	474	13	AAQ24442	Encodes truncated
0.7	29.	4	5870	77	AAA15044	Nucleotide sequenc
41	12.	ď	339	19	AAV19804	Truncated sTNFR, s
42	10.	ď	462	13	444	Encodes truncated
43	98	ď	333	19	AAV19805	
44	304.4	ď	332	13	æ	Truncated sTNFR, s
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Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-IR; fusion protein; linker; TNF: IL-1; cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allografit; xenografit; rejection; graft verses host disease; sepsis; inflammation; allergy; AAQ49932 standard; cDNA to mRNA; 1368 BP Location/Qualifiers
1..1366
1..1366
4.tag a /product hTNF-R
1..120
/*tag b /*tag b /*tag c c autoimmune dysfunction; ss 29-APR-1994 (first entry) Lambda-derived INF-R cDNA. Lambda-gt10-7-ctnfbp. Homo saptens sig_peptide mat_peptide AAQ49932; Key

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                                                                                                                                                                                                                                                                                                                                                     The Inker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion protien is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosis and assays for conditions mediated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft and xenograft rejection in graft verses host disease, sepsis, septic shock, inflammation, allergies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTCCTGGAGCTGTTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                          The sequences given in AAQ49931-32 encode human tumour necrosis fireceptor (INF-R) and the sequences in AAQ49933-34 encode human interleutin-1 receptor (IL-1R). These sequences were used in the production of a fusion protein which conformed to one of the formulae:
                                                                                                                                                                protein tumour necrosis factor and human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 14; Length 1368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                             receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1366.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                 TNF-R-11nker-TNF-R-11nker-IL-1R
IL-1R-11nker-TNF-R-11nker-TNF-R OF
TNF-R-11nker-TNF-R
                                                                                                                                                                                                                      Disclosure; Page 57-59; 85pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.98;
           93WO-US02938
                                       92US-0860710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               st Local Similarity 99.9 tches 1367; Conservative
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                                                                                                                                      P-PSDB; AAR42059
                                                                 IMMA ) IMMONEX
                                       30-MAR-1992;
                                                                                                                                                               New fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TGCAGGGAGTGTGAGAGGGGTCCTTCACCGCTTCAGAAAACCACCTCAGACACCTCTC
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                                                                                                                                                                                                                                                                                         0; Gaps
  biological function of TNFR1 and identifying drugs targeting the protein for treating disorders -
                                                                                                                                                                                                                                                              Score 1366.4; DB 21; Length 1368;
Pred. No. 0;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                    Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T; 0 other;
                                         Claim 7; Fig 4; 79pp; English.
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Best Local Similarity 99.9%;
Matches 1367; Conservative
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                         TNFR1; tumour necrosis factor receptor; polymorphism; human;
tumour; cancer; apoptosis; bacterial infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chew A;
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                                                                                           Cocation/Qualifiers
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                                                                                                                      /*tag= a
/product= "TNFR1"
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replace(224,T)
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Human TNFR1 coding sequence.
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SCHULZ V P.
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                                                                         The sequence encodes the entire 30 kD TNF inhibitor. The clone from which the sequence was obtd. was isolated from a cDNA library prept. from RNA form 0937 cells treated with PMA/PHA. The whole gene can be inserted inco expression vectors for prepn. of TNF inhibitor for use in the treatment of inflammatory and degenerative
                                                                                                                                                                      DB 12; Length 2088;
                              of TNF-alpha
                                                                                                                                                                                         ö
                                                                                                                                                                                         1; Indels
                                                                                                                                                     T; 0 other;
                               suppression
                                                                                                                                                                                                                    Query Match
99.9%; Score 1366.4;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches
                                                                                                                                                    Sequence 2088 BP; 439 A; 626 C; 578 G; 445
                                                                                                                                  See also AAQ10878, AAQ10884 and AAQ10907
                             our necrosis factor inhibitor - for -beta, useful as therapeutic agent.
                                                        Disclosure, Fig 21; 142pp; English
  WPI; 1991-073847/11
          P-PSDB; AAR10986
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171..1536
/*tag= a
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89US-0381080.
89US-0450329.
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                                                                                             The present invention relates to Tumour Necrosis Factor (TNF) inhibitors dee AAB37676 and AAB37685), which have Thr Inhibitory activity. The novel TNF inhibitors of the present invention are useful as therapeutic agents for inhibiting the activity of TNF and interleukin (IL-1), and for treating inflammatory and degenerative diseases mediated by TNF. The present sequence is the coding sequence for the precursor of 30 kDa TNF inhibitor can inhibit TNF alpha.
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                                                                                                                                                                                                                                                          GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTGGATTTGCTGTACC
                                                                                                                                                                                                                                                                                                                                          AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTGTTGCACAGTGGAC
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                                                                                                                                                                                                                                                                                                                                                                   TGCAGGGAGTGTGAGGGGCTCCTTCACCGCTTCAGAAACCACCTCAGACACTGCCTC
                                Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and degenerative diseases mediated
                                                                                                                                                                                     DB 22; Length 2088;
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                                                                                                                                                                   Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;
                                                                                                                                                                                                      <del>;</del>
                                                                                                                                                                                    Similarity 99.9%; Score 1366.4; Similarity 99.9%; Pred. No. 0; 7; Conservative 0; Mismatches
                                                                             82pp; English
       WPI; 2001-006443/01.
P-PSDB; AAB37677.
                                                                             Example 6; Fig 21;
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Best Local Simi
Matches 1367;
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                                                                                                             GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCCATCCCCAACCCCCTTCAGAAG
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                                                                                                                                                                                                                                                                                                                                        TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; LL-1; inflammatory disease; degenerative disease; human;
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Kohno T;
                                                                                                                                                                                                                                                                                                                                                                                             ВР
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Vanderslice RW, Vannice J, Ko
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93US-0090366.
89US-03B1080.
89US-0450329.
90US-0479661.
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11-DEC-1989;
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This invention describes novel homogeneous insoluble proteins (I), their (in)soluble fragments (Ia) and their salts that can bind tumour necrosis factor (TNF). The products of the invention have anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i) to treat diseases in which TNF is involved (e.g. septic shock, autoimmune glomerulonephritis, cerebral malaria, immune responses and inflammation), (ii) to purify TNF, (iii) to identify TNF (ant)sponists and (iv) for diagnostic determination of TNF in body TNF inlds sequence encodes (I) are used for affinity purification of (I). This sequence encodes a tumour necrosis factor binding protein described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGAGCTGTTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199.9%; Score 1366.4;
11arity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
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89CH-0003319.
90CH-0000746.
                                                     90EP-0116707
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P-PSDB; AAY30934.
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Best Local Similarity
Matches 1367; Conserv
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                                                                                              20-APR-1990;
12-SEP-1989;
08-MAR-1990;
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Schlaeger E;
                                                     31-AUG-1990;
       01-SEP-1999.
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(in)soluble fragments and pharmaceutically acceptable salts, able to bind tumor necrosis factor (TMF) and in homogeneous form. The products of the invention have antinflammatory, immunosuppressive, antibacterial, antiprotozoal activity. (I), and related recombinant proteins, are used antiprotozoal activity. (I), and related recombinant proteins, are used to treat diseases mediated by TMF. e.g. shock in cases of meningococcal sepsis; development of autoimmune glomerulonephritis and cerebral malaria. Also (I), or antibodies specific for them, are used for diagnostic determination of TMF in body fluids, for affinity purification of TMF and for identifying (anniagonists of TMF. This sequence encodes a human TMF binding protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New homogeneous, insoluble proteins that bind tumor necrosis factor (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
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99.9%; Score 1366:4; DB 22; Length 2111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0: 0
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                                                                          "TNFBP-associated protein"
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Location/Qualiflers
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90CH-0001347.
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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
                                                                                                     Human; 88; granulocytic cell; DNA chip; bacterial infection, viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                   Human cDNA differentially expressed in granulocytic cells #610.
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                    ABK84039 standard; cDNA; 2111
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                                                              (first entry)
                                                                                                                                                                                                                                                                                                           (GENE-) GENE LOGIC INC.
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                                                                                                                                                                                                     Homo sapiens.
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                                                              14-AUG-2002
                                         ABK84039;
RESULT 7
ABK84039
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Claim 1; SEQ ID No 610; 114pp; English.

The invention relates to detecting (MI) granulocyte (GC) activation CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by CC CC MA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated CC the control of a control of GCA.

Also included are modulating (MX) GA by contacting GCA with an agent that alters the expression of at least one gene in Gs; (2) screening (MX) for an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; where CC the level of expression of the gene is indicative of inflammation; (4) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. MI is useful for detecting at issue having condulating GA mislammation in a tissue, an allergic effecting an inflammation in a tissue, while susful for screening an agent capable of modulating condulating GA preferably in an inflammation in a tissue, an allergic effecting an inflammation of especially chronic) in a tissue, an allergic effecting an inflammation of especially chronic) in a tissue, an allergic effecting an inflammation of especially chronic) in a tissue, an allergic effecting an inflammation of especially chronic) in a tissue, an allergic effecting an inflammation of especially chronic) in a tissue, an allergic effecting an inflammation of especially chronic) in a tissue, an allergic effecting an inflammatory disease (e.g. psoriasis, rheumatoid arthritis, gonerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, Φ

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parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                             Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T;
                                                                                               Score 1366.4;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 1367; Conservative
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                                                                                                                                                                                                                                                         The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver
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GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCCTTCAGAAG
                                                                                                                                  GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCCTTCAGAAG
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                                                                                                                                                               Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease sti disease progression; drug toxicity; drug efficacy; drug metabolism.
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tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, error forcilly, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIDO at fip.WIDO.int/pub/published_pct_sequences.
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The invention provides antisense compounds targeted to human tumour necrosis factor receptor type I (TNRR1) RNA. These antisense compounds can be used in a method of inhibiting the expression of TNRR1 human cells or tissues. The antisense compounds specifically hybridize with one or more nucleic acids encoding TNRR1 modulating the function of nucleic acid molecules encoding TNRR1 ultimately modulating the amount of TNRR1 produced. The antisense compounds and method are useful as research reagents and diagnostics, and in the treatment and prophylaxis of infection, inflammation or tumour formation. The present sequence represents the nucleotide sequence of human TNRR1 (GenBank Accn No: X55313).
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                                                                                                                                                                                                                                   This invention relates to a novel method for enhanced killing of tumour cells comprising contacting a tumour cell with a synergistic cells comprising contacting a tumour cell with a synergistic combination of a death domain receptor ligand and a diterpenoid triepoxide. This method has cytostatic activity and works by blocking triepoxide. This method has cytostatic activity and works by blocking TNP-alpha mediated induction of c.IAP2 and c.IAP1. The method of the invention may be used for treating tumours, particularly solid tumours, e.g. carcinoma, mammary adenocarcinoma and non-small cell lum carcinoma also neurological malignancies, non-Wite cutaneous T-cell lymphoma, cutaneous T-cell ymphomatoid papulosis, T-cell rich cutaneous T-cell lymphoma, lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasis, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered with other active agents, e.g. antimetastatic, anti-tumour or anti-angiogenic agents. The potent synergy between the diterpenoids and the death domain ligands allows increased xilling at equivalent or lower doses, and can sensitise otherwise resistant cells. This sequence represents the human tumour necrosis. factor alpha receptor (TNF-RI) DNA. TNF-RI is a death domain receptor used in the used method of the invention in combination with diterpenoid triepoxides to kill tumours by inducing apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1366.4; DB 24; Length 2161;
Pred. No. 0;
0; Mismatches 1; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;
                                                                                                                                                                                                           Disclosure; Column 23-28; 20pp; English
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990S-149989P
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Matches 1367; Conservative
                                (STRD ) UNIV LELAND
                                                                                                    WPI; 2002-121125/16.
P-PSDB; AAU75064.
                                                                 Rosen GD, Kao P;
20-AUG-1999;
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             TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                           Partial amino acid sequences were determined for the 55 and 75kD TNF-BPB (see AAR11072-R11081) and oligonucleotide primers were synthesised based on these partial sequences. The primers were used to produce a cDNA fragment for use as aprobe to screen a human placental cDNA bank constructed in lambda 9t11. Positive clones were identified and sequenced. DNA constructs comprising the TNF-BP coding sequence may also contain a fragment encoding a human Ig domain. Recombinant constructs are used to transform cells to confer improved TNF-binding properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 2111;
                                                                                                                                                                                                                                                                                              Insoluble tumour necrosis factor binding proteins - and DNA encoding them, useful in pharmaceutical prods. and for antibody prodn.
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Pred. No. 0;
0; Mismatches
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      Location/Qualiflers
187..273
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                                                                                                                                                              90CH-0001347.
89CH-0003319.
90CH-0000746.
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Best Local Similarity 99.9%;
Matches 1366; Conservative
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                                                                                                                                                                                                                                   Brockhaus M,
Schlaeger EJ;
                                                                                                                                                             20-APR-1990;
12-SEP-1989;
08-MAR-1990;
                                                                                                                                        31-AUG-1990;
                     sig_peptide
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                                                                                                                                                                                                                                                                                                                           p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera; epidermal growth factor receptor; EGF-R; protease; inhibitor; phorbol myristate acetate; PMA; ss.
                                                                                                                                                                                                                                                                               New protease capable of cleaving soluble tumour necrosis factor (TNP) receptor - from cell-bound TNF- receptor, useful for antagonising deleterious effects of TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 2175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T; 0 other;
                                                                                                                                                                                                                                           Wallach D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be used for enhancing TNF function.
                                                                                                                                             "possible poly. A signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1364.8;
Pred. No. 0;
                                                                                                                                                                                                                                          Varfolomeev E,
                                                                                            Location/Qualifiers
256..1623
256..1623
/tag= a /product= p55 TNF-R
2143..2149
/tag= "possible poly
                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 40pp; English
                                                                                                                                                                                                                          RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.8%;
                                                                                                                                                                                           . 94AU-0075742
                                                                                                                                                                                                           93IL-0107268
               19-JAN-1996 (first entry)
                                                                                                                                                                                                                                         Batkin M, Brakebusch C,
                                                                                                                                                                                                                                                        WPI; 1995-194342/26.
P-PSDB; AAR75084.
                               p55 TNF-R gene.
                                                                                                                                                                                                                          (YEDA ) YEDA
                                                                                                                                                                                           11-OCT-1994;
                                                                                                                                                                                                          12-OCT-1993;
                                                                               Homo sapiens
                                                                                                                                                            AU9475742-A
                                                                                                                                                                           04-MAY-1995
                                                                                                                              misc_signal
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AAQ90513;
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9 855 099 915 720 975 780

1095 1155 1215 1020 1080 1035 900 960 840 1036 GGAACTACTAACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACCACCCAGGTTCACC CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAAGAGGTGGCACCACCTATCAGGG GGAACTACTACTAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC CCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGGTGGCACCACCCTATCAGGGG GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCCTTCAGAAG TGGGAGGACACCCCCACAAGCCACACAGACCTAGACACTGATGACCCCGCGACGCTGTAC 1276 à

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GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAGA 120
                                                                                                    AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAATCTCTTCTTGCACAGTGGAC
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                                                                                                                                     GATAGTGTGTGTCCCCAAGGAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC
                                                                                                                                                                          CGGGACACCGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT
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                                                                                          1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG
                                                                          Gaps
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useful for treating diseases where TNF alpha is involved as a causative agent, e.g. cachexia, sepsis and autoimmune diseases
                                                       Length
                                                                        3; Indels
                                    Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T; 0 other;
           causative agent, e.g. cachexia, sepsis and autoimmune specifically rheumatoid arthritis. See also AAQ20974.
                                                       DB 13;
                                                     Score 1363.2;
Pred. No. 0;
                                                                        0; Mismatches
                                                     99.68;
                                                               Best Local Similarity 99.8
Matches 1365; Conservative
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                                            TACAGCATGCTGGCGACCTGGAGGCGCGCGCGCGCGGGGGCGCGAGGCCACGCTGGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of DNA encoding tumour necrosis factor alpha binding protein which was obtd. from a human placental cDNA library in lambda gtll using a probe (AAQ20974). The DNA also encodes the extracellular domain of human TNF alpha receptor and as such it is
                                                                                                                                                                                                                                                                                                                                                                                                                extracellular domain of human
                                                                                                                                                                                                                                                      Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss; extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New tumour necrosis factor alpha binding protein and polypeptide - useful in treating cachexia, sepsis and auto immune diseases
                                                                                                                           CTTTGCGGCCCCGCCCTCCCGCCCGCGCCCAGTCTTCTCAGATGA 1368
                                                                                                                                                                                                                                                                                                   /note= "encodes the extracornotes TNF alpha receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-043613/06.
P-PSDB; AAR20787.
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       SUNLEY RES CENT
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                                      WPI; 1992-167156/20.
P-PSDB; AAR24000.
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                       Brennan FM,
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                     GCTGACCCCATCCTTGCGACAGCCCTCGGCCTCCGACCCCATCCCCAACCCCCTTCAGAAG 1174
                                                                               CTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGGCG 1320
                                                                                                                                                                                       CTGGGACGCGTGCTCCGCGACATGGACCTGCTGGCTGCCTGGAGGACATCGAGGAGGCG 1474
                                               1355 TACAGCATGCTGGCGACCTGGAGGCGGCGCCGCGGGGGCGGGGGCCACGCTGGAGCTG
                                                                                                               TACAGCATGCTGGCGACCTGGAGGCGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTG
      GCTGACCCCATCCTTGCGACAGCCCTCGCCTCCGACCCCCATCCCCAACCCCCTTCAGAAG
                                      TGGGAGGACAGCCCCACAGCCCACAGAGCCTAGACACTGATGACCCCGCGACGCTGTAC
                                                                                                                                                                                                                                                                                                                              tumour necrosis factor alpha; extracellular binding domain; treatment; pulmonary diseases; septic shock; HIV infection; AIDS; malaria; viral meningits; graft versus host disease; autoimmune disease; richemand darthrits.
                                                                                                                                                                                                                1475 CTTTGCGGCCCCGCCCCCCCCCCCCCCCCCCCAGTCTTCTCAGATGA 1522
                                                                                                                                                                                                       CTTTGCGGCCCCGCCCTCCCGCCGCGCCCAGTCTTCTCAGATGA 1368
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/product- human TNF-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq:"TGG", aa:Thr
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156..1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon- Seq"AAG",
                                                                                                                                                                                                                                                                                                               Encodes TNF-alpha 55kD receptor.
                                                                                                                                                                                                                                                                DNA; 2062
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                                                                                                                                                                                                                                                                                  This sequence encodes human TNF-alpha 55kD receptor . A placenta CDNA library in gt10 was screened with probe AAQ29236. Ten hybridising clones were plaque purified and CDNA size determined by PAGE against an ECO RI digested phage DNA. The inserts of two CDNA clones were then sequenced. The coding region of the majority of the human TNF-alpha 55kD receptor was isolated as an ECORI fragment encoding 374 amino acids, and cloned into a mammalian cell expression vector, resulting in priNRR. A derivative of the TNF-alpha receptor was produced by engineering a termination codon just prior to the transmembrane engineering a termination codon just prior to the transmembrane restriction fragment which was cloned into priNRR, giving pINFReed. DNA sequencing confirmed this contained the designed DNA sequence.
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                                                                                                                                New polypeptide capable of binding human TNF alpha - comprises first three cysteine-rich subdomains of TNF alpha receptor for treating autoimmune disease, septic shock, HIV etc.
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  Turner MJC;
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99.6%; Score 1363.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1365; Conservative 0; Mismatches
  Gray PW,
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Feldmann M,
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us-09-899-422a-1.rng

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The Tumour Necrosis Factor Binding Protein I is the soluble form of type I TNF-receptor and constitutes a fragment of the cell surface form of this receptor, corresp. to its extracellular domain. There is no characteristic poly(A) addition signal near the 3' end of the cDNA. The sequence ACTAAA (tag m) may serve as an alternative to this signal, but with low efficiency. See also AAQ1212-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant tumour necrosis factor binding protein I - prepd. by transfecting eukaryotic cells with vector contg. deoxyribonucleic acid encoding human type I TNF receptor or soluble domain
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kemper O, Engelmann H, Brakebusch C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T; 0 other;
  te= "in-frame termination codon"
..1620
                                                                                                                                                                      /*tag= g
/note= "TBP-I derived sequence"
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"TBP-I derived sequence"
                   /*tag= a
/product= type I TNF receptor
256..318
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/label= transmembrane_domain
885..504
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89IL-0092697.
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757..858
/*tag= 1
/number= 4
2145..2150
/*tag= m
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P-PSDB; AAR12550.
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13-DEC-1989;
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  TGGGAGGACCCCCACACAGCCACAGAGCCTAGACACTGATGACCCCGCGACGCTGTAC 1080
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                                                          995 CCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCACCTCCACCTATACC
                                                                                                                                                                                                        GCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTG
                                   CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGGCACCACCCTATCAGGGG
                         AATGTTAAGGGCACTGAGGACTCCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT
                                                                                            GGAACTACTACTAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

eic - nuc	search, using sw model
Run on: Ju	June 8, 2003, 22:32:19; Search time 3520 Seconds (without alignments) 11310.409 Million cell updates/sec
Title: US Perfect score: 13 Sequence: 1	US-09-899-422A-1 1368 1 atgggcctctccaccgtgcccgcccagtcttctcagatga 1368
Scoring table: ID	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched: 20	2054640 segs, 14551402878 residues
Total number of hi	hits satisfying chosen parameters: 4109280
Minimum DB seq len Maximum DB seq len	length: 0 length: 200000000
Post-processing: M	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	Gen Embl: * 11 90 ba: * 21 90 bhtg: * 22 90 bhtg: * 33 90 bits: * 43 90 bat: * 54 90 bat: * 55 90 bat: * 65 90 bat: * 66 90 bat: * 76 90 bh: * 86 90 bat: * 87 90 bit: * 88 90 bat: * 89 90 bat: * 80 bat: * 8

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		A29098 Synthetic D	M63121 Human tumor	HOM	ASSASS HUMAN TUMOI	AX409713 Segmence	M58286 Homo sapten	AR096330 Sequence	A55313 H. saptens T	A78738 Sequence 7	AR041076 Sequence	164751 Sequence 1	Algyd/ Synthetic n	AZISZZ INF ALPHA 9 I43805 Sequence 24	A20255 55kD recept	AK056611 Homo sapi	M6U2/5 Human tumor A29103 H sapiens m	AB051103 Fells cat	.019994 Sus scrofa	AF329976 Rattus no.	AX401925 Sequence	M63122 Rat tumor n	AF329978 Rattus no	AF329980 Rattus no	AF329981 Rattus no	M59377 Murine tumo	X59238 Murine mRNA	BC004599 Mus muscu	L26349 Mus musculu	MS//96 MOUSE MKNA	AR031375 Sequence	Compos1	126928 Sequence 2 A20257 Synthetic n	Sequence	310 Sequenc	AR134762 Sequence A21525 oliaopucleo			linear PAT 03-JUL-1995 tent EP0393438.					,I. and Stratowa,C. DNA coding therefor	G.M.B.H
SUMMARIES DB ID	- ;		9 HUMTNFRC			6 AX409713									6 A20255		S A29103							10 AF329980					MUSTNFX	PTIME PTITO		BD000		14380	AR131	6 A21525	ALIGNMENTS		1368 bp DNA TNF-receptor from patent	,		ott.		<pre>Hauptmann, R., Himmler, A., Maurer-Fogy, TNF-receptor, TNF-binding protein and Patent: EP 0393438-A 48 24-0CT-1990;</pre>	EIM INTERNATIONAL G.M
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/traislation="MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVC
PQGKYIHPQDNSICCTKCHKGTYLXNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
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GRCLREAQYSMLATWRRTPRREATLELLGRVLRDMDLLGCLEDIEEALCGPAALPPA
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mRNA, complete
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Molecular cloning and expression of human and rat tumor factor receptor chain (p60) and its soluble derivative, necrosis factor-binding protein
DNA Cell Biol. 9 (10), 705-715 (1990)
                                                                                                                                                                                                                                                                                                                           CTTGCGGCCCGCCGCCCCCCGCCGCCCGGTTCTCTCAGATGA 1368
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Mammalia; Eutheria; Primates; Catarrhin; Hominidae; 1
1 (bases I to 2112)
Himmler,A., Maurer-Fogy,I., Kronke,M., Scheurich,P.,
Pfizenmaier,K., Lantz,M., Olsson,I., Hauptmann,R., St.
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tumor necrosis factor receptor
Human CDNA to mRNA.
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207. .1574
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Location/Qualifiers
1. 1368
/organism="synthetic construct"
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1424 c 375 g 276 t
                                                                                        100.0%; Score 1368; DB 6
100.0%; Pred. No. 1e-265;
1ve 0; Mismatches 0
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http://www.nisc.nih.gov/
Contact:
nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,F., Legaspl,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Zhang,L.-H. and Green,E.D.
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1 (bases 1 to 2194)
Strausberg, R.
Direct Submission
Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
GCTGACCCCATCCTTGGGACAGGCCTCGCCTCCGACCCCATCCCCAACCCCTTCAGAAG
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                                                                                                                                                                                                     cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Galthersburg, Maryland:
Web site:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1 (bases I to 2087).

Schall, T.J., Lewis, M., Koller, K.J., Lee, A.L., Rice, G.C., Wong, G.H., Gatanaga, T., Granger, G.A., Lentz, R., Raab, H., Rohr, W.J. and Gooddel, D.V.

Molecular cloning and expression of a receptor for human tumor necrosis factor
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Series: IRAL Plate: 27 Row: m Column: 22
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 339755.
Location/Qualifiers
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/db_xref="LocusID:/132"
/db_xref="taxon:9606"
/clone="MGC:19588 IMAGE:4131360"
/tlssue_type="Muscle, rhabdomyosarcoma"
/clone_ilb="NHR_MGC_17"
/lab_host="DH10B-R"
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Brockhaus M., Dembic, Z., Gentz, R., Lesslauer, W., Loetscher, H. and
Schlaeger, B.J.
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/organism="synthetic con/db_xref="taxon:32630"
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/codon_start=1
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Draft entry and computer-readable sequence for [1] kindly submitted
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Pred. No. 2.1e-265;
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/db_xref-"taxon:9606"
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PQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC
SKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE
                                                           KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPOIENVKGTEDSGTTVLLPLVI
FFGLCLLSLLFIGLMYRYQRMKSKLYSIVCGKSTPRREGELEGTTTRFLAPNFSFSPT
PGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPI
PNPLQXWEDSAHKPQSLDTDDPATLYAVVENVPPLRRKEFVRRLGLSDHEIDRLELQN
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/product="55 kD TNF-BP"
/protein_id="CAA01805.1"
/db_xref="G1:904969"
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Loetscher, H., Pan, Y.C., Lahm, H.W., Gentz, R., Brockhaus, M.,
Tabuchi, H. and Lesslauer, W.
Molecular cloning and expression of the human 55 kd tumor necrosis
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/db_xref-*G1:3724*
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FFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPT
PGFTPTLGFSPYPSSFFTSSGTYTPGDCPNPRARRYAPREVAPOKGADPTLATALASDPT
PNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRGLSDHEIDRLELQN
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forms of tumor necrosis factor receptors (TNF-Rs), The type I TNF-R, cloned using amino acid sequence data of form, encodes both the cell surface and a soluble form
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Nophar, Y., Kemper, O., Brakebusch, C., Englemann, H., Zwang, R., Aderka, D., Holtmann, H. and Wallach, D.
                                                                                                     TCCAAGCTCTACTCCATTGTTGTGGGAAATCGACACCTGAAAAAGAGGGGGGGCCTTGAA
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(S Wallach, D. Brackebusch, C., Varfolomeev, E. and Batkin, M. Proteases capable of shedding the soluble TNF-receptor and TNF-R derived peptides and antibodies against the proteases inhibiting the shedding 1065756-A 114-JUN-1995;

YEBA RES & DEV (IL)
Other publication ZA 9407962 951121
Other publication AV 7574294 950504
Other publication AV 7574294 950504
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//organism="unidentified"
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FEATURES Location/Qualifiers source 1. 2175 /unidentified" Ad_xref="taxon:32644" ORIGIN	Query Match 99.9%; Score 1366.4; DB 6; Length 2175; Best Local Similarity 99.9%; Pred. No. 2.1e-265; Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps		121 GATAGTGTGCCCAAGGAAATATATCCACCTCAAAATAATTGGATTTGGACCCTCAAGGACAGGACAGGACAGGACAGAGACAGAGAGAAATATTGGACCCTCAAGAAAAAAAA		Db 436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGCTCCAGGCCGGGGCAGGATACGGAC 495 Qy 241 TGCAGGAGGTGAAGGGGCTCCTTCACCGCTTCAGAAACCACCTCAGACACTGCCTC 300	Db 496 TGCAGGGGTGTGGTTCCTTCACCGCTTCAGAAAACGACTTCAGAAAACGCCCTC 555 Oy. 301 AGCTGCTCCAAAGGAAATGGGTGGTGGAGTGCTCTTCTTGCACGTGGAC Oy. 111111111111111111111111111111111111	556 361	Db 616 CGGGACACCGTGTGTGCGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675 Qy 421 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACTCTCCTGCCAGGAG 480	Db 676 TICCAGTGCTTCAATTGCAGCCTCGCCTCATGGGACCGTGCACCTCCTCCTCCTCCTGCAGGAG 735 OY 481 AAACAGAACACGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGT 540	Db 736 AAACAGAACCGTGTGCACTGCATGCTTTCTTAGAAAAAACGAATGTC 795 QY 541 TCCTGTAGTAACTGTAAAAAAAAAAAGAAAAGGAGTGGGGGGGG	796 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTTGTTGTTGTTGTGTTGTGTTGTGTTGTGTTGTGTGTGT	Db 856 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCTTTTTTTT	OY 721 TCCAAGCTCTACTCCATTGTTGGGAAATCGACACCTGAAAAGGGGGGGG		Db 1096 CCCACCTGGGCTTCAGCCGTGCCCATCCTCCACTTCAGCTCCACTTTTTTTT	OY 901 CCCGGGGACTGTCCCAACTTTGCGGGTCCCCCGAGAGGTGGCACCACCTATCAGGGG 960
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Oy 541 Db 796 Oy 601	Db 856 Qy 661		1	Oy 841 Db 1096	Oy 901 Db 1156	QY 961 Db 1216		Qy 1081 Db 1336	Qy 1141 Db 1396	Oy 1201 Db 1456		Gy 1321 Db 1576	, v	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	ΑΓ

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241 TGCAGGGAGTGGAGGGGCTCCTTCACGAAACCACCTCAGACACTGCCTC 300	481 AAACAGAACACGGGGGCATGCAGGTTCTTTCTAAGAGAAAACGAGTGTGC 540 11	721 TCCAAGCTCTACTCCATTGTGGGAAATCGACACCTGAAAAGGGGGGAGCTTGAA 780	1021 TGGGAGGCCCCCACAAGCCCACAGCCTAGACCTGATGACCCCGCGACGCTGTAC 1080
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Expression of the recombinant tumor necrosis factor binding protein
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Wallach, D., Nophar, Y., Kemper, O., Engelmann, H., Brakebusch, C. and
Aderka, D.
                                                                                                                                                                                                                                       1176 TGGGAGACAGCCCCCACAAGCCACAGACCTAGACACTGATGACCCCGCGACGCTGTAC
           GCCGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTG
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Synthetic nucleotide sequence Type I TNF receptor gene.
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Patent: US 5665859-A 1 09-SEP-1997;
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Wallach,D., Brakebusch,C., Varfolom
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/db_xref="GI:579600"
/db_xref="SMISS-PROT-19438"
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RQNTVCTCHAGFFLENRCVSCSNCKRSLECTRLCLPOIENVRGTEDSGTTVLLPLVI
PFGLCLILSILFIGLATRRYQRRKSRLYSIVCKRSTPRREGELEGTTTRFLAPNPSFSPT
PGFTPTLGGFSVPVSSTYTFGSSTYTFGCDPPATLYANVENPPLRREFYRRLGSDHITATALASDPI
PNPLORWEDSAHKROGELDTDDPATLYANVENPPLRREFYRRLGSDHEIDRLELQN
GRCLERAQYSMLATWRRRFFRREATLELLGRVLRDMDLIGGLEDIEERALCGPAALPPA
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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OM protein - nucleic search, using frame_plus_p2n model
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2487 1 MGLSTVPDLLLPLVLLELLV......DIEEALCGPAALPPAPSLLR 455 16154066 seqs, 8097743376 residues Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-09-899-422A-2 **BLOSUM62** Title: Perfect score: Sequence: Scoring table: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

32308132

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

parameters: Command line

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-UB-/cgn2_1/USPTO_spool/US09899422/runat_04062003_145737_14712/app_query.fasta_1.647
-UB-/cgn2_1/USPTO_spool/US09899422/runat_04062000
-USRR-dS09899422_cdn2_1_12874_erunat_04062003_145737_14712_-NGDE-LOCAL
-USRR-GS09899422_cdn1_12874_erunat_04062003_145737_14712_-NGDU-6_-ICPU-3
-NO_MMAP_IARGEQUERY_NGG_SCORES-0_WAIT_-DSPBLOCK-100_-LONGLOG
-USRR-USUT-120_-WARN_TIMEOUT-30_-THREADS-1_-XGAPOP-10_-XGAPEXT-0.5_-FGAPOP-6
-FGAPEXT-7_-YGAPOP-10_-YGAPEXT-0.5_-DELEXT-7

ESI: * Database :

em_gss_other:* em_gss_mam:* em_gss_mus:* em_gss_pro:* em_gss_rod:* em_gss_hum:• em_gss_pln:* em_gss_fun:* em_estfun: em_gss_vrt em_estom: * em_esthum: em_estba:* em_estmu em_estov: em_estpl em_estro: gb_est2 b_est3 gb_est5 gb_gss: b_est4 gb_est1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

BQ723672 AGENCOURT_8489850 Lupski_dorsal_root_ganglion Homo sapiens CDNA clone IMAGE:6184295 5', mRNA sequence.		Homo sapiens Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 931)	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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p mRNA 1_root_gang	1	Cranlata; <v Caterrhini;</v 	/. Mammalian
931 bj pski_dorsa 5', mRNA se	569	Chordata; (Primates; (ci.nih.gov, of Health,
BQ723672 AGENCOURT_8489850 Lupsk1_dorsal_root_g clone IMACE:6184295 5', mRNA sequence.	BQ723672 BQ723672.1 GI:21862569 EST. human.	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteler Ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 931)	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Ma
BQ723672 AGENCOURT clone IMA			NIH-MGC h
RESULT 1 BQ723672 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE	ORGANISM REFERENCE	AUTHORS

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178 GluCysValSerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuPro
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/dev_stage="adult, 36 yr"
/lasue_type="adult, 36 yr"
/lab.host="best="billob"
/lab.host="billob"
/note="vector: power SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5'-TCGACCAGCGCGCGCGG; and the following adaptors:
5'-TCGACCAGCGCGCGG; and the following adaptors:
1 kb for average insert length 1.7 kb. This is a primary library, non-amplified Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Linl at:
http://image.lln.gov
Plate: LiaMi3573 row: d column: 24
High quality sequence stop: 607.

Location/Qualifiers
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Contact: cusscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

Location/Qualifiers
1. .957

/Organism="Homo sapiens"
//Organism="Homo sapiens"
//Organism="Homo sapiens"
//Organism="Homo sapiens"
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//Clone="CsObator: 9606"
//Clone="CsObator: PLI_NFL008_TC2"
//Clone=Lib="LTI_NFL008_TC2"
//Clone=
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prime, mRNA sequence.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 957)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Uppublished (2001)

Contact: Genoscope
                                                                                                                                                                                                                                                                                422 GAGTGTCTCCTGTAGTAACTGTAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCC
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PheSerProValProSerSerThrPheThrSerSerSerThrTyrThrProGlyAspCys
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                                      1.4e-125
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Note: this is a NIH_MGC Library." ORIGIN Alignment Scores: 7.89e-114 Length: 741 Score: 1292.00 Matches: 241 Best Local Similarity: 98.78 Mismatches: 2	51.95% Indels: 13 Gaps: 455) x B1860918 (1-741)	Oy 87 GlySerPheThralaSerGluAsnHisLeuArgHisCysLeuSerCysSerLysCysArg 100	Oy 107 LysGluMetGlyGlnValGluIleSerSerCysThrValAspargAspThrValCysGly 126	Qy 127 CysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeuPheGlnCysPhèAsnCys 146	Oy 147 SerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCys 166	Oy 167 ThrCysHisalaGlyPhePheLeuArgGluAsnGluCysValSerCysSerAsnCysLys	Qy 187 LysSerLeuGluCysThrLysLeuCysLeuProGlnIleGluAsnValLysGlyThrGlu	Qy 207 AspserGlyThrThrValLeuLeuProLeuVall1ePhePheGlyLeuCysLeuLeuSer 226	Qy . 227 LeuLeuPheileGlyLeuMetTyrargTyrGlnargTrpLysSerLysLeuTyrSerIle 24	Qy 247 ValCysGlyLysSerThrProGluLysGluGlyGluLeuGluGlyThrThrLysPro 266	Qy 267.LeuAlaProAsnProSerPheSerProThrProGlyPheThrProThrLeuGlyPheSer 286	Qy 287 ProValProSerSerThrPheThrSerSerThrTyrThrProGlyAspCysProAsn 306	Oy 307 PheAlaProArgArgGluValAlaProProTyrGln-GlyAlaAspProIleLeuAl 3	Qy 326 aThralaLeuala 330 ::: Db 722 GACAAGCCTCGCT 734	RESULT 5 BM546826 LOCUS BM546826 LOCUS BM546826 DEFINITION AGENCOURT_6491128 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723557 5, mRNA sequence.
314 TTCAGTCCCGGGCCCAGTTCCACCTTCACCTCCACCTATACCCCCGGTGACTGT 373 305 ProAmnPheAlaAlaProArgArgGluValAlaProProTyrGlnGlyAlaAspProIle 324	AlaHisLysProGluSerLeuAspThrAspAspProAlaThrLeuTyrAlaValValGlu 364 	365 AsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisGlu 384 	385 IleaspargLeuGluLeuGlnasnGlyargCysLeuargGlualaGlnTyrSerMetLeu 404 	AlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeuLeuGlyArgVal 424 	LeuArgAspNetAspLeuLeuGlyCysLeuGluAspIleGluGluAlaLeuCysGlyPro 444 	445 AlaAlaLeubroproAlaproSerLeuLeuArg 455 	741 bp mRNA linear EST 10-OCT-2001	⊣	zoa; Chordata; Craniata; Vertebrata; Daimata; Daimata; Daimata;	<pre>Manualist is Littleria; Filtheria; Catalinii; Hominidae; Homo. 1 (bases 1 to 741) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Inpublished (1909)</pre>	Confect: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nlh.gov Tissue Procurement: DCTD/DTP	CDNA Library Preparation: Lite Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be	found through che 1.M.A.G.E. CORBOTTIUM/LENL AT: http://image.llnl.gov Plate: LLAM12017 row: h column: 21 High quality sequence stop: 740.	1. 711 /organism="Homo sapiens" /db_xref="taxon:9606"	/clone="IMAGE:339108" /clone=lib="NH_MGC_87" /tlssue_itype="nammary adenocarcinoma, cell line" /tlssue_type="nammary adenocarcinoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 1 383 kh library contiched for

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AU131978 NT2RP3 Homo sapiens cDNA clone NT2RP3003570 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genomics@hri.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH1sTyrTrpSerGluAsnLeu
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                                                         566 CGGGACACCGTGTGTGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGACAACCTT
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HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yama, Kilsarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3986
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/lab_host="DH10B*
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036.* 1 others
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bassa 1 to 1070)

1 (bassa 1 to 1070)

1 (Dublished (ttp://mgc.nci.nih.gov/.

1 Unpublished (1999)

2 Contact: Robert Strausberg, Ph.D.

2 Email: Gapbs.remail.nih.gov

Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: NGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence start: 2

High quality sequence stop: 669.

Location/Qualifiers

1. 1070

//db_rref="texton:9606"
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//db_rref="texton:9606"
//db_rref="texton:9606"
//db_rref="texton:9606"
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4 others
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cells after 2-weeks retinoic acid
n 199 c 201 g 179 t 4
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AL529836 LTI_NFL001_NBC4 Homo sapiens cDNA brine, mRNA sequence.

AL52836

AL52836

GI:12793329
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Matches:
Conservative:
Mismatches:
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/lab_host="bH10B"
/lab_host="DH10B"
/lab_host="DH10B"
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was primed with a NotI-oligo(dT) primer. Five prime end
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cloned into the Not I and Eco RV sites of the pCNVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : filang@lifetech.com URL :
http://fullength.invitrogen.com" 3 others
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          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 942)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM10185 row: g column: 20
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/clone_lib="LTI_NEUGE_PL2"
/tissue_type="Placenta"
/tissue_type="Placenta"
/note="WeetOr: pCMVSDORT 6; Site_l: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco Rv sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com"
http://fullength.invitrogen.com"
8 258 c 259 g 221 t 6 others
                                                                                                                                                                                                                                                             AL577008 LIL_NFL006_PL2 Homo saplens cDNA clone CSODI082XA01 5 prime, mRNA sequence.

AL577008 I GI:12939716
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                        LysGlnAsnThrValCysThrCysHisAlaGly-PhePheLeuArgGluAsnGluCysVa
                                                                          180 lSerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGl
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                 975
232
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4
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Onpublished (2001)
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Matches:
Conservative:
Mismatches:
Indels:
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/clone="CSODIO82YA01"
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96.27%
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// Soganism="Homo sapiens"

/organism="Homo sapiens"

/organism="Homo:9606"

/clone="IMAGE:531041"

/clone="Lib="NHIE MGC_71"

/tissue_type="leiomyosaccoma"

/tab_host="bill0" (phage-resistant)"

/note="Organ: uterus; Vector: pcNv-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2.1 kb. 3 others
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
L (bases 1.0 994)
L Unpublished (1999)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
                                                                                                                                                                                                                                                     994 bp mRNA linear EST 05-MAR-2002
5', mRNA sequence.
                                          660 CTTTTGCCTTTTATTCCTCCTCTTCAGIGGCGTAAAIGTAGTCGCTGCCACGCGGAAGCC 719
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                             241 rLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGluGl
                                                                                  261 yThrThrThrLysPro-LeuAlaProAsnProSerPheSerProThrProGlyPheThrP
                                                                                                                                      281 roThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThrP
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1211.50
87.06%
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                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/tissue_type="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma, cell line"
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Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for full length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library.*
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Matches:
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High quality sequence stop: 657 Location/Qualifiers
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         Contact: Takeo 1sogai

Genomics Laboratory

Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Tel: 81-438-52-3976

Tel: 81-438-52-3976

Email: genomics@thi.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute of Medical Science, University of Tokyo, and

Helix Research Institute.
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                                                                                                                                                                                                                                     others
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                                                                                                                                      l...889
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                                         CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
                                                                                                                                             AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTCTAAGAGAAAACGAGTGTGTC 705
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Catarrhini, Hominidae, Homo.
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Eukaryota; Metzzoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 889)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y.; Nagai,T., Sugano,S. and
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                       GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGGACAGGAGAGAA
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Homo sapiens cDNA clone HEMBA1001229 5'
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BG680679 718 bp mRNA linear EST 01-MAY-2001 02626965F1 NCI_CGAP_SKn4 Homo sapiens cDNA clone IMAGE:4751536 5',
                                                                                       ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrp-SerGluAsnLe 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CLOR distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM10608 row: b column: 17
High quality sequence stop: 679.
Incertain Constitution 
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Hammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 718)
NIH-MGC http://mgc.ncl.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
                           41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone_lib="Organ: brain; Vector: pCMV-SPORT6; Site_l: Not1;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dr
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC_Library.

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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
E I (bases I to 916)
S NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Consortium (LLNL)
DNA Sequencing by: Tncyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llol.gov
Plate: LLAM11500 row: f column: 06
High quality sequence stop: 827.
Location/Qualifiers
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603029519F1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5199749 5',
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                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5kb. Library constructed by Life Technology. Note: this is a NCI_CGAP Library."

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Mismatches:
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Matches:
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BM742388 65NU620 Homo sapiens cDNA clone S6SNU620-5-C12 5',
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 669)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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Korea Research Institute of Bioscience & Biotechnology
52 Ecoun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Biate: 5 row: C column: 12
High quality sequence stop: 669.
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Mismatches:
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Unpublished (2002)
Contact: Kim YS
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Best Local Similarity:
                                      BM742388
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 837)

E 14, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

AL Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY codex - France

Email: sequefégenoscope.cns.fr. Web : www.genoscope.cns.fr.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  AL522989

AL522989 I.TL_NFL004_NBC2 Homo sapiens CDNA clone CSODB009YP14 5 prime, mRNA sequence.

AL522989.1 GI:12786482
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           1..837
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/clone="Lib="LTI_NFL004_NBC2"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH100"
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AUTHORS
TITLE
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LOCUS
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vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Librang Life Technologies. a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 http://fullengellfetech.com/URL: http://fullengellfetech.com/URL: 1231 c 229 g 177 t lothers
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Copyright (c) 1993 - 2003 Compugen Ltd.
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1 atgggcctctccaccgtgcc.......sgcccagtcttctcagatga 1368 US-09-899-422A-1 1368 Perfect score: Scoring table: Sequence:

441362 segs, 153338381 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

1: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
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6: /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Issued_Patents_NA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 3, Appli Sequence 3, Appli Sequence 53, Appli Sequence 3, Appli Sequence 3, Appli Sequence 49, Appli Sequence 49, Appli Sequence 13, Appli Sequence 51, Appli Sequence 51, Appli Sequence 11, Appli Sequence 1, Appli
US-08-804-166-3 US-08-910-991-3 US-08-050-3198-53 US-08-465-982-3 US-08-465-982-3 US-08-465-982-3 US-08-465-982-3 US-08-465-982-4 US-09-397-787-236 US-09-397-787-236 US-09-397-787-236 US-09-397-787-236 US-08-050-3198-51 US-08-050-3198-51 US-08-928-069-11 US-08-928-069-11 US-08-928-069-11 US-08-928-069-11 US-08-928-069-11 US-08-928-069-11 US-08-928-069-11 US-08-928-069-11 US-08-928-069-11 US-08-928-069-11 US-08-928-683A-9 US-08-915-469-3 US-08-915-469-3 US-08-915-469-3
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ALIGNMENTS

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US/09106038A Baker and Lex M. Cowsert EXPRESSION 91 SI ATTISENSE MODULATION OF THFRI SI ATTION Windows NT T Word 97 ATA: US/09/106,038A 26, 1998 ATION: Bernstein 137,280 MBER: RTS-0004 MBER: RTS-0004 MBER: RTS-001 131-9200 131-9200 131-9200 131-9200 11-1CS:	DB 3;	CCACTGG1 	CCTCACC
M. Cowsert Inc. Mb	Score 1366.4; Pred. No. 0; 0; Mismatches	SCTGCTG	ACTGGTC
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                                                                                                                               MEDIOM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                 ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
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Pred. No. 0;
0; Mismatches
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APPLICATION NUMBER: US/08/321,668
APPLICATION WIMBER: US/08/321,668
CLASSIFICATION 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 12-007-1993
APPLICATION NUMBER: IL 107268
FILING DATE: 12-007-1993
ATORNEY AGENT INFORMATION:
REFERENCE/DOOKET NUMBER: 25,618
REFERENCE/DOOKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-628-5197
TELEFAX: 202-628-5197
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Best Local Similarity 99.9%;
Matches 1367; Conservative 0
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
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STRANDEDNESS: single
                                                                                             ZIP: 20004
COMPUTER READABLE FORM:
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                  TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCCAGAGTTGTGCCTACCCCAGATTGAG
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Patent No. 565859
Patent No. 565859
Patent No. 565859
APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: VARFOLOMEEV, Eugene
APPLICANT: VARFOLOMEEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE TUF RECEPTORS, THEIR PREPARATION AND THEIR INUMBER OF SEQUENCES: 42
                                                                                                                                             CTTTGCGCCCCGCCCCCCCCCCCCCCCCAGTCTTCTCAGATGA 1368
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TITLE OF INVENTION: THE THE RECEPTORS, THEIR PREPARATION AND THEIR USE NUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

CONPUTER: Floppy disk

CONPUTER: DEAD COMPATIBLE

CONPUTER: DEAD COMPATIBLE

CONPUTER: PATENTY

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/837,941

FILING DATE: 28-APR-1997

CURRESIFICATION: 4.35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                     E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1366.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,668
FILING DATE: 12-007-1994
APPLICATION NUMBER: II-107268
FILING DATE: 12-007-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-13
TELECHOME: 202-628-5197
TELECHAN: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                         TELERX: 202-/s, -
TELERX: 248633
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDENESS: single
STRANDENESS: linear
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99.98;
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Best Local Similarity 99.9
Matches 1367; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 256..1620
                                  ADDRESSEE: BROWDY
STREET: 419 Seven
CITY: Washington
STATE: D.C.
COUNTRY: USA
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                                     1036 GGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC
                                                                          TCCTGTAGTAACTGTAAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG
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Sequence 1, Application US/08837941
Patent No. 5766917
GENERAL INCOMMATION:
GENERAL TO APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARFOLOMEEV, Eugene
APPLICANT: WARTIN, MACCHAET
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF

RESULT 4 US-08-837-941-1

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256 ATGGGCCTCTCCACCGTGCCTGCTGCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG
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                          APPLICANT: ENGELMANN, HARTMUT
APPLICANT: BRAKEBUSCH, CORD
APPLICANT: ADERKA, DAN
TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                      COMPUTER: 200ABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,016
FILING DATE: 24-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                         E: Browdy and Nelmark
419 Seventh Street, N.W., Suite 300
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/625668
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION UNBER: 25,618
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELERX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: NUCLEIC acid
STRANDENNESS: SINGIE
                                                                                                                                                                                                                                                                                                                                                                                                            25,618
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  NOPHAR, YARON
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256..1620
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                KEMPER,
                                                                                                                                                     Washington
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LOCATION:
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US-08-126-016-1
                                                                                                                                                  CITY: Was
STATE: DC
                                                                                                                                      STREET:
                APPLICANT:
APPLICANT:
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Best Local (
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CGGGACACCGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675
                                                                                                                                   GGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACC
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Patent No. 3811261
GENERAL INFORMATION:
APPLICANT: WALLACH, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-126-016-1
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TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 256..1620
                                                                                                                                    COUNTRY:
  RESULT 6
US-08-054-970-1
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                   556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTGCACAGTGGAC
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                                                                                                                  AAACAGAACACCGTGTGCCATGCCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC
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COMPUTER READABLE FORM:
MEDITUR TREADABLE FORM:
MEDITUR TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/054,970
FILING DATE: 03-MAY-1993
CLASSIFICATION: 435
                                         GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
TITLE OF TWORTION: THE RECEPTOR ACTION MODULATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
99.9%; Score 1366.4;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches
                                                                                                                                                                           ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W. CITY: Washington STATE: D.C.
Sequence 1, Application US/08054970 Patent No. 6395267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: TOWNSENG, KEVIN G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHAN: 202-737-3528
```

1: Floppy disk IBM PC compatible

3: Reed & Robbins 635 Bryant Street

USA

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COPERATION SYSTEM: PC-DS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTONEX/AGENT INFORMATION:
NAME: RODDINS, RODERTA L.
RECISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1902
TELEPAX: (415) 617-8999
TELEFAX: (415) 327-3231
       GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human Thralpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA to mRNA FEATURE:
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                                                                                                                                         ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
COMPUTER: IBM PC COMO
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                                                                                                             CITY: Palo Alto
STATE: California
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Patent No. 5633145
                                                                                        ADDRESSEE:
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RESULT 7 US-08-050-319B-24 ; Sequence 24, Application US/08050319B

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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPTER: IBM PC compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
FILING DATE: US/08/465,982
FILING DATE: US/08/050,319
  Modified human TNFalpha (Tumor
Necrosis Factor alpha) Receptor
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TITLE OF INVENTION: Modified DITLE OF INVENTION: Necrosis NUMBER OF SEQUENCES: 57 CORRESPONDENCE ADDRESS: ADDRESSE: Reed & Robbins STREET: 635 Bryant Street CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                         ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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; LOCATION: 155..1519
US-08-465-982-24
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ö 180 240 300 454 360 214 334 574 8 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTGGATTTGCTGTACC AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 1 ATGGGCCTCTCCACCGTGCCTGCTGCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTGCACAGTGGGAC CGGGACACCGTGTGTGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT Gaps ö Length 2062 Indels ະດ .. 301 455 361 515 ò 셤 à 셤

GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan

Sequence 24, Application US/08465982 Patent No. 5863786

RESULT 8 US-08-465-982-24

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CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
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                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILLOATION NUMBER: US/08/762,308 FILLING DATE: 09-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 690.4; DB 2;
Pred. No. 3.3e-156;
0; Mismatches 351;
                                                                                                                                                                                                                                                                                                                        NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:335--1
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/224,593
FILING DATE: 05-ARR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION TELEPHONE: 418-3000
                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 474-7577
TELEFAX: 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCÉ CHARACTERISTICS:
LENGTH: 1956 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.5%;
                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.5
Best Local Similarity 72.2
Matches 975; Conservative
                                              ADDRESSEE: Arnold, Wh. STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                 COMPUTER READABLE FORM:
                                                         STREET: P.O. BOX CITY: Houston STATE: TX COUNTRY: USA ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                  MEDIUM TYPE:
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Flavia M.
MODIFIED RECEPTORS THAT CONTINUOUSLY
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                                                                                                                                                               Length 2440;
                                                                                                                                                                                       Indels
                                                                                                                                                                Score 685.4; DB 4;
Pred. No. 5.6e-155;
                                                                                                                                                                                      0; Mismatches 326;
                                                4.0
 CURRENT FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 60/122,156
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FESTSEQ FOR Windows Version
SEQ ID NO 1
LENGTH: 2440
                                                                                                                                                              Query Match 50.1%;
Best Local Similarity 71.1%;
Matches 1021; Conservative
                                                                                                                              ; LOCATION: (294)...(1706)
US-09-513-007-1
                                                                                TYPE: DNA ORGANISM: Bos taurus
                                                                                                                  NAME/KEY: CDS
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                                                                                           GGAAAGCCCCTAACT----CCAGCCCCTCCCCAGCCTTCAGCCCCACTCCGGCTTC
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                                                                              GAGAATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTC
                                                                                                                           TTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGG
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OF USE
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Patent No. 6466907
GENERAL INFORMATION:
APPLICANT: Taylor, J. Michael
APPLICANT: Kehrli, Jr., Marcus
APPLICANT: Lee, Eun-Kyung
APPLICANT: Mwangi, Simon
TITLE OF INVENTION: BOVINE TUMOR NECROSIS FA
TITLE OF INVENTION: AND METHODS OF USE
TITLE REFERENCE: 08411-018001
CURRENT APPLICATION NUMBER: US/09/513,007
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                                                                                                                                                                                                                                           Length
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Pred. No. 3e-142;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08286740
Patent No. 5561053
GENERAL INFORMATION:
APPLICANT: CTOWNEY, CTAIG W.
TITLE OF INVENTION: HOST CELLS
NUMBER OF SEQUENCES: 4
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: CB1016
TELECOMUNICATION INFORMATION:
TELEPRONE: 619-410-8926
TELEFAX: 619-410-8928
                                                                                                                                                                                                                                         46.3%;
                                                                                                          INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 6896 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.7
Matches 634; Conservative
                                                                                                                                                                                             linear
                                                                                                                                                                                           ; TOPOLOGY:
US-08-627-151A-6
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US-08-286-740-2
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                                                                             CCCGGTGACTGTCCCAACTTTGCGGCTCCCCGCAGAGGTGGCACCACCCTATCAGGGG
                                                                                                                                           Sequence 6, Application US/O8627151A
Patent No. 5866341
GENERAL INFORMATION:
APPLICANT: STINGLIA, Dominic
APPLICANT: STINGLIA, Dominic
APPLICANT: BECHERER, Kathleen
APPLICANT: BECHERER, Kathleen
APPLICANT: STINGNN, Steven
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: SCREENING DRUG LIBRARIES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: Gen-Frobe Incorporated
STREET: 10210 Genetic Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEMO FOR Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,151A
FILING DATE: 03-APR-1996
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CAMPUTER: IBM COMPATIBLE
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APPLICATION NUMBER:
FILING DATE:
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STATE:
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Pred. No. 3.7e-142;
0; Mismatches 1;
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                                                                                                                                                                                                     601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09576
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT GENERATECH, INC.
TITLE OF INVENTION: METHOD FOR SELECT
TITLE OF INVENTION: HOST CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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ama: 798PCT
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APPLICATION NUMBER: 08/286740
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 798PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9509576 GENERAL INFORMATION:
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Best Local Similarity 99.8:
Matches 633; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 6889 bases
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                 MEDIUM TYPE: 5.25 inch, 360 kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/286,740
FILING DATE: 05-AUG-1994
CLASSIFICATION 0435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy W.
REGISTRATION NUMBER: 798
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 910/311-7168
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 6889 bases
                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roPoLOGY: linear
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61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGAA 120
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                                   Length 600;
                                                                       Indels
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Patent No. 5863786
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.W. Brennan
TITLE OF INVENTION: Modified human INFalpha (Tumor TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
                                   DB 1;
                                  Score 593.6; DB 1;
Pred. No. 3.4e-133;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
                                  Query Match 43.4%;
Best Local Similarity 99.3%;
Matches 596; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
US-08-050-319B-47
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                                                                                     301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 360
                                                                                                                                                             CGGGACACCGTGTGTGCCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 420
                 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
                                                                                                                                                                                Sequence 47, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human ThFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTX: USA

ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 617-8999
TELEFRANT ON SEQ ID NO: 47;
SEQUENCE CHARACTERISTICS:
TENGENTY FOR SEQ ID NO: 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 634
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TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION:
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GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAAAGAGA 120
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Pred. No. 3.4e-133;
0; Mismatches 4;
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
MITORNEY/AGENT INFORMATION:
NAME: RODDINS, RODGITA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                          43.48;
                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                       Query Match 43.4
Best Local Similarity 99.3
Matches 596; Conservative
                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 1..597
US-08-465-982-47
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Search completed: June 9, 2003, 01:14:09 Job time: 97 secs

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9, 2003, 01:17:59; Search time 185 Seconds (without alignments) 3442.105 Million cell updates/sec
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2487
1 MGLSTVPDLLLPLVLLELLV......DIEEALCGPAALPPAPSLLR 455
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                      OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                       870385 segs, 699768693 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

fasta_1.647

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/cgn2_6/ptodata/2/pubpna/US07_BNB_PUB.seq:*
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//cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli
SUMMARIES	sult Query No. Score Match Length DB ID	US-09-898-234-1 US-09-899-429A-1 US-09-792-356-1 US-09-899-422-1
	BG	9999
	Query Match Length DB	1368 1368 1368 1368
di	Query	100.0 100.0 100.0
	Score	2487 2487 2487 2487
	Result No.	H 44 W 44

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ALIGNMENTS

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### APPLICANT: Hammler, Adolph
### APPLICANT: Hammler, Adolph
### APPLICANT: Hammler, Adolph
### APPLICANT: Hammler, Adolph
### APPLICANT: Maurer-Fogy, Ingrid
### APPLICANT: Maurer-Fogy, Ingrid
### APPLICANT: Stratowa, Christian
### TITLE OF INVENTION: Them
### TITLE OF INVENTION NUMBER: 08/38,676
### PRIOR FILING DATE: 1992-02-01
### PRIOR FILING DATE: 1992-02-01
### PRIOR FILING DATE: 1993-11-17
### PRIOR FILING DATE: 1993-01-02
### PRIOR FILING DATE: 1990-04-20
### PRIOR
Sequence 1, Application US/09898234
Patent No. US20020155112A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
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                               LOCATION: (1)..(1368)
NAME/KEY: 819_peptide
LOCATION: (1)..(87)
NAME/KEY: misc_feature
LOCATION: (88)..(120)
OTHER INFORMATION: extracellular proteases following secretion.
NAME/KEY: misc_feature
LOCATION: (606)..(633)
                                                                                                 LOCATION: (606)..(633)
OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion.
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Matches:
Conservative:
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Best Local Similarity:
         Homo
                 FEATURE:
NAME/KEY: CDS
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US-09-898-234-1
TYPE: DNA ORGANISM: 1
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GENERAL INCORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Amaurer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: Them
TITLE OF INVENTION OWBER: 08/099,429A
CURRENT APPLICATION NUMBER: 08/192,356
PRIOR FILING DATE: 1995-06-07
PRIOR PILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
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PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 97
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Patent No. US20020169118A1
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720 260

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Sequence 1, Application US/09792356
Publication No. US20020183485A1
GENERAL INFORMATION:
Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauter, Adolph
APPLICANT: Hauter, Adolph
TITLE OF INVENTION: The Receptors, TNF Binding Proteins and DNAs Coding for TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
CURRENT APPLICATION NUMBER: US/09/792,356
CURRENT FILING DATE: 1995-00-01
PRIOR PLING DATE: 1995-00-01
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1990-04-20
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SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 1368
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 319_Peptide
LOCATION: (1).. (87)
NAME/KEY: misc_feature
LOCATION: (88).. (120)
OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion
NAME/KEY: misc_feature
LOCATION: (86).. (633)
OTHER INFORMATION: extracellular proteases following secretion
OTHER INFORMATION: extracellular proteases following secretion
OTHER INFORMATION: extracellular proteases following secretion
CS-09-899-429A-1
                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Sequence 1, Application US/09899422

Patent No. US2020009676a1

GENERAL INFORMATION:

APPLICANT: Hummler, Adolph
APPLICANT: Hummler, Adolph
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
CURRENT APPLICATION NUMBER: US/09/899,422
CURRENT ELING DATE: 2001-08-21
PRIOR FILING DATE: 2000-03-15
PRIOR PELLING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-01-02

PRIOR PLICATION NUMBER: 08/153,287
PRIOR PLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-01-02

PRIOR APPLICATION NUMBER: 07/821,750

PRIOR PLICATION NUMBER: 07/821,750

PRIOR APPLICATION NUMBER: 07/821,750
                                                                            601 AATGTTAAGGGCACTGAGGACTCAGGCACACAGTGCTGTTGCCCCTGGTCATTTTCTTT
                            GlyLeuCysLeuLeuSerLeuLeuPhelleGlyLeuMetTyrArgTyrGlnArgTrpLys
                                                                                                                              GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr
                                                                                                                                           ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr
                                                                                                                                                                                              ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly
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                                            TYPE: DNA
ORGANISM: Homo saplens
ORGANISM: Homo saplens
ORGANISM: Homo saplens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1368)
NAME/KEY: sig_peptide
LOCATION: (1)..(67)
NAME/KEY: misc_feature
LOCATION: (88)..(120)
OTHER INFORMATION: Portion of TWF-BP pro protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion.
LOCATION: (606)..(633)
OTHER INFORMATION: extracellular proteases following secretion.
COTHER INFORMATION: extracellular proteases following secretion.
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Matches:
Conservative:
Mismatches:
Indels:
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2487.00
100.00%
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NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1368
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Best Local Similarity:
Query Match:
DB:
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Sequence 2360, Application US/09880107

Patent No. US20020142981A1

GAPPLICANT INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: GAPPLICANT: GAPPLICANTON: GAPPLICANTON: GAPPLICANTON NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE PATENT OF SEQ ID NOS: 3950

SOFTWARE PATENT OF SEQ ID NOS: 3950
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                                                       TYPE: DNA
ORGANISM: Homo saplens
FETURE:
NAME/KEY: CDS
LOCATION: (1)..(1368)
NAME/KEY: sig_peptide
LOCATION: (1)..(87)
NAME/KEY: misc_feature
LOCATION: (88)..(120)
OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion.
NAME/KEY: misc_feature
LOCATION: (606)..(633)
OTHER INFORMATION: extracellular proteases following secretion.
COTHER INFORMATION: extracellular proteases following secretion.
COTHER INFORMATION: extracellular proteases following secretion.
US-09-899-422-1
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Mismatches:
Indels:
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Matches:
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2487.00
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PRIOR FILING DATE: 1990-04-20
NUMBER OF SED ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SED ID NO 1
LENGTH: 1368
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Best Local Similarity:
Query Match:
DB:
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                     AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu
                                                                                                                                                            AlaaspProlleLeualaThralaLeualaSerAspProlleProAsnProLeuGlnLys
                                                                                                        TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Artificial Sequence: human TNF-R in
                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/09898234

Sequence 16, Application US/09898234

Sequence 16, Application US/09898234

SERENAL INFORMATION:

APPLICANT: Humler, Adolph

APPLICANT: Humler, Adolph

APPLICANT: Humler, Adolph

APPLICANT: Stratowa, Christian

TITLE OF INVENTION: Them

TITLE OF INVENTION: Them

TITLE OF INVENTION: Them

STILE REFERENCE: 98,385-1

CURRENT APPLICATION NUMBER: US/09/898,234

CURRENT FILING DATE: 2001-07-03

PRIOR PAPLICATION NUMBER: 08/525,998

PRIOR APPLICATION NUMBER: 08/153,287

PRIOR PILING DATE: 1995-02-01

PRIOR APPLICATION NUMBER: 07/821,750

PRIOR PILING DATE: 1990-04-20

SEQ ID NO 16

LENGHARE: PATENTING VET: 2.0

SEQ ID NO 16

LENGHARE: PATENTING NUMBER: 07/821,430

PRIOR FILING DATE: 1990-04-20

SEQ ID NO 16

LENGHARE: PATENTING NUMBER: 07/821,430
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OTHER INFORMATION: Description
OTHER INFORMATION: 1TNF-R2
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Pred. No.:
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US-09-880-107-2360
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	QY 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 7 US-09-099-429A-26 Sequence 26, Application US/09899429A Sequence 26, Application US/09899429A Sequence 26, Application US/09899429A Patent No. US20020169118A1 GENERAL INFORMATION: APPLICANT: Humler, Adolph APPLICANT: Humler, Adolph APPLICANT: Aurer-Fogy, Ingrid APPLICANT: Attoowa. Christian TITLE OF INVENTION: Them TITLE OF INVENTION: Them FILE REFERENCE: 98-385-J CURRENT FILING DATE: 2001-07-03 PRIOR APPLICATION NUMBER: US/09/99,429A PRIOR APPLICATION NUMBER: 09/792,356	PRIOR APPLICATION NUMBER: 08/477, 639	ORGANISM: Artificial Sequence FEATURE FORTURE FEATURE FORTURE FO
Matches: 455 100.00% Conservative: 0 5 5 5 5 5 5 5 5 5	1 AspSerValCysProGlnGlyLysTyrlleHisProGlnAsnasnSerileCysCysThr 1 (11111111111111111111111111111111111	101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120	81 SerCysSerAsnCysLysLysSerLeuGluCysThrIysLeuCysLeuProGlnIleGlu	TACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGAGGGGGACACTALLYSProlating of the control of

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                                                                                                                                                                                                                                                                                                                    ## STENERAL INNOMANTION:
## STENERAL INNOMANTION:
## APPLICANT: Hauptmann, Rudolph
## APPLICANT: Hauptmann, Rudolph
## APPLICANT: Hauptmann, Rudolph
## APPLICANT: Hauptmann, Rudolph
## APPLICANT: Hauptmann, The Receptors, TNF Binding Proteins and DNAS
## TITLE OF INVENTION: The Receptors, TNF Binding Proteins and DNAS
## TITLE OF INVENTION: The Receptors, TNF Binding Proteins and DNAS
## CURRENT APPLICATION NUMBER: US/09/792,356
## CURRENT FILING DATE: 1995-06-07
## PRIOR PELING DATE: 1995-06-07
## PRIOR FILING DATE: 1995-06-07
## PRIOR FILING DATE: 1993-11-17
## PRIOR PELING DATE: 1993-11-17
## PRIOR PELING DATE: 1992-01-02
## PRIOR FILING DATE: 1992-01-02
## PRIOR FILING DATE: 1990-04-20
## NUMBER OF SEQ ID NOS: ## PRIOR FILING DATE: 1990-04-20
## NUMBER OF SEQ ID NOS: ## PRIOR FILING DATE: 1990-04-20
## NUMBER OF SEQ ID NOS: ## PRIOR FILING DATE: 1990-04-20
## SOFTWARE: PatentIN Ver. 2.0
## SEG ID NO 16
## TENNOW: 2141
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Publication No. US20020183485A1
GENERAL INFORMATION:
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NAME/KEY: CDS
LOCATION: (213
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	Oy 401 TyrSerMetLeuAlaThrTpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420	Oy 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla 440		RESULT 9 US-09-899-422-16 ; Sequence 16, Application US/09899422 ; Patent No. US20020090676A1	; GENERAL INFORMATION: ; APPLICANT: Hauptmann, Rudolph ; APPLICANT: Himmler, Adolph ; APPLICANT: Maurer-Fogy, Ingrid	; APPLICANT: Stratowa, Christian ; TITLE OF INVENTION: The Receptors, TNF Binding Proteins and DNAS Coding for ; TITLE OF INVENTION: Them ; FILE REFERENCE: 98,385-H	CURRENT APPLICATION NUMBER: US/09/899,422 CURRENT FILING DATE: 2001-08-21 PRIOR FILING DATE: 2000-03-15	; PRIOR APPLICATION NUMBER: 08/383,676 ; PRIOR FILING DATE: 1995-02-02 ; PRIOR APPLICATION NUMBER: 08/153,287 ; PRIOR FILING DATE: 1993-11-17	; PRIOR APPLICATION NUMBER: 07/821,750 ; PRIOR FILING DATE: 1992-01-02 ; PRIOR APPLICATION NUMBER: 07/511,430 ; PRIOR FILING DATE: 1990-04-20	; NUMBER OF SEQ ID NOS: 87 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 16 ; LENGTH: 2141	; TYPE: DNA ; OKGANISM: Artificial Sequence ; FEATURE: ; NAME/KEY: CDS	: LOCATION: (1580) : OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in oTHER INFORMATION: 1TNF-R2 US-09-899-422-16	1.14e-250 Length: 2487.00 Matches:	Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 10 Gaps: 0	US-09-899-422A-2 (1-455) x US-09-899-422-16 (1-2141) Qy 1 MetGlyLeuSerThrValProAspLeuLeuLeuValLeuLeuGluLeuLeuVal 20	AIGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCTGGTGCTCCTGGAGCTGTTGGTG	Qy 21 GlylleTyrProSerGlyVallleGlyLeuValProHisLeuGlyAspargGluLysArg 40	Oy 41 AspSerValCysProGlnGlyLysTyrlleHisProGlnAsnAsnSerlleCysCysThr 60
21 GlylleTyrProSerGlyVallleGlyLeuValProHisLeuGlyAspArgGluLysArg 40 	41 AspSerValCysProGlnGlyLysTyrIleHiSProGlnAsnAsnSerIleCysCysThr 60 	61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyGlnAspThrAsp 80 	GluasnHisLeuargHisC 	101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120 	121 ArgAspThrValCysGlyCysArgLysAsnGlbTyrArgHisTyrTrpSerGluAsnLeu 140 	141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160 	161 LysGlnAsnThrvalCysThrCysH1sAlaGlyPhePheLeuArgGluAsnGluCysVal 180 	181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGln11eGlu 200 	201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValllePhePhe 220 	221 GlyLeuCysLeuLeuSerLeuLeuPheileGlyLeuMetTyrArgTyrGlnArgTrpLys 240	241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260 	261 GlyThrThrThrLysProLeualaProAsnProSerPheSerProThrProGlyPheThr 280 [111111111111111111111111111111111111	281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr 300 	301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320 	321 AlaAspProlleLeuAlaThrAlaLeuAlaSerAspProlleProAsnProLeuGlnLys 340 	1 TrpGluAspSerAlaHisiysProGluSerLeuAspThrAspAspProAlaThrLeuTyr	seasgaraguguucaaaguuaaguutagaaguutagaraguugagaagaagaagaagaagaagaagaagaagaagaag	1293 GCGTGGTGGAGAACGTGCCCCGTTGCGCTGGAAGGAATTCGTGCGGCGCCTAGGGCTG 1352 381 SeraspHisGluileAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400

Qy 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla 440	Patent No. US20020142357A1 GENERAL INFORMATION: SENERAL INFORMATION: PAPLICANT: WALLACH, David BRAKEBUSCH, Cord TITLE OF INVENTION: INF RECEPTOR ACTION MODULATION	NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W. CITY: Washington STATE: D.C.	COMPUTE: USA COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS	SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/120,397 FILING DATE: 12-Apr-2002	; PRIOR APPLICATION: GURGOWD> ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US/08/054,970 ; FILING DATE: 03-MAY-1993	ATIORARY AGENT INFORMATION: MAME: Townsend, Kevin G. REGISTRATION NUMBER: 34,033 REFERENCE/DOCKET NUMBER: WALLACH-9	TELEPHONE: 202-628-5197	SEQUENCE CHARACTERICS: SEGUENCE CHARACTERICS: LENGTH: 2175 base pairs TYPE: nucleic acid	STRANDENESS: SINGLE STRANDENESS: SINGLE TOPOLOGY: linear MOLECULE TYPE: ONA FEATURE:) NAME/KEY: CDS ; LOCATION: 256.1620 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-120-397-1		ity:	-09-899-422A-2 (1-455) x US-10-120-397-1 (1-2175)	Qy I MetGlyLeuserinivalProAspleuLeuleuval 20
LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAsp1	513 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTTCTTGCACAGTGGAC 572 121 ATGASPThrValCy9GlyCy8ATGLy8AsnGlnTyTATGH15TyrTrpSetGluAsnLeu 140	141 PhedlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160 	693 AACAGACACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	201 AsnValLysGlyfhrGluAspSerGlyfhrThrValLœuLœuProLeuValIlePhePhe 220 	221 GlyLeucysLeuLeuSerLeuLeuPhelleGlyLeuWetTyrargTyrGlnArgTrpLys 240 	241 SerLysLeutyrSerileValCysGlyLysSerthrProGluLysGluGlyGluLeuGlu 260 	261 GlythrthrthrLysProLeuAlaProAsnProSerPheSerProThrProGlypheThr 280 	281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300 	301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320 	321 AlaAspProileLeuAlaThrAlaLeuAlaSerAspProileProAsnProLeuGinLys 340 	341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360 	361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380 	381 SerAspHisGluileAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400	

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1516 CTGGGACGCGCGCCCCGCGACATGGACCTGCCTGGCTGCCTGGAGGACATCGAGGAGGCC 1575
                               TACAGCATGCTGGCGACCTGGAGGCGGCGCACGCCGCGGGCGCGAGCTG 1515
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            TyrSerwetleualaThrTrpargargargThrProargargGlualaThrLeuGluLeu
                                                      LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla
                                                                                                                                                                                        GURBEAL INFORMATION:
TILLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
FILE REFERENCE: A-71992
CURRENT APPLICATION NUMBER: US/10/252,408
CURRENT FILING DATE: 2002-09-24
PRIOR PELING DATE: 1994-06-08
PRIOR FILING DATE: 1994-06-13
PRIOR PELING DATE: 1999-05-10
PRIOR FILING DATE: 1989-09-11
PRIOR FILING DATE: 1989-09-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VUMBER: US 07/403,241
PRIOR FILING DATE: 1989-09-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3
LENGTH: 1368
                                                                                                           441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
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                                                                                                                                                           Sequence 3, Application US/10252408
Publication No. US20030082736A1
GENERAL INFORMATION:
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99.78%
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FEATURE:
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; LOCATION: (1)..(120)
; OTHER INFORMATION:
US-10-252-408-3
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LOCATION: (121)..()
OTHER INFORMATION:
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LOCATION: (1)..(1365)
OTHER INFORMATION:
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Best Local Similarity:
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Sequence 11, Application US/09898234

Patent No. US20020155112A1

GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Haumler, Adolph
APPLICANT: Mauter-Fogy, Ingrid
APPLICANT: MAURER-FOGY, Ingrid
APPLICANT: MAURER NE Receptors, TNF Binding Proteins and DNAS Coding for
TITLE OF INVENTION: Them
FILE REFERENCE: 98,385.
CURRENT APPLICATION NUMBER: 09/25,998
FRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 1993-01-07
PRIOR PRILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                            LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
           GlylleTyrProSerGlyValileGlyLeuValProHisLeuGlyAspArgGluLysArg
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OTHER INFORMATION: Description of Artificial Sequence: CDNA insert of CTHER INFORMATION: LambdaTNF-BP15 and pTNF-BP15 vectors US-09-898-234-11
                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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100.00%
83.19%
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Best Local Similarity:
Query Match:
DB:
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SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
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                LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp
                                                                                       CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu
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; OTHER INFORMATION: Description of Artificial Sequence: (
; OTHER INFORMATION: LambdafNF-BP15 and pINF-BP15 vectors
US-09-792-356-11
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                      US/09/792,356
TITLE OF INVENTION: Them
CURRENT APPLICATION NUMBER: US/09/792,3
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 08/477,639
PRIOR FILING DATE: 1995-06-07
PRIOR PELING DATE: 1995-06-07
PRIOR PELING DATE: 1995-02-01
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PARENTIN VET: 2.0
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LENGTH: 1334
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APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: TWE Receptors, TWF Binding Proteins and DNAS Coding for
                                                                  872
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Publication No. US20020183485A1
GENERAL INFORMATION:
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qa	1233		Qy	3 101
Qy	361	AlavalvalGluAsnvalProProLeuArgTrpLysGluPhe 374	qq	513 A
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RES	RESULT 14		qa	573 0
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	TITLE OF I	binding froceins and bans couring	ΟŽ	181 S
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	PRIOR APPL	No DAIL: 2000 03-13 ICATION NUMBER: 08/383,676	Ωp	813 A
•• ••	PRIOR APPL		λō.	221 G
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	NUMBER OF	SEQ ID NOS: 877	đ	933 T
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RMATION: Description of Artificial Sequence: cDNA insert PRMATION: lambdaTNF-BP15 and pTNF-BP15 vectors
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41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60	Oy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120 11	Qy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160 111111111111111111111111111111111111	Qy 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGinileGlu 200	Oy 221 GlyLeuCysLeuLeuSerLeuLeuPhelleGlyLeuMetTyrArgTyrGlnArgTrpLys 240	Oy 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280		arch completed: June 9, 2003, 02:44:47
Oy 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320	Qy 361 AlavalValGluAsnValProProLeuArgTrpLysGluPhe 374 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GENERAL INFORMATION: APPLICANT: Hauptmann, Rudolph APPLICANT: Haumler, Adolph APPLICANT: Haurer-Fogy, Ingrid APPLICANT: Stratowa, Christian TITLE OF INVENTION: THE Receptors, TNF Binding Proteins and DNAs Coding for FILE REPERENCE: 98-385-J	T APPLICATION NUMBER: US/09/899,429A T FILING DATE: 2001-07-03 APPLICATION NUMBER: 09/792,356 FILING DATE: 2000-02-23 APPLICATION NUMBER: 08/477,639 FILING DATE: 1955-06-07 FILING DATE: 1955-06-07 FILING DATE: 1955-06-07 FILING DATE: 1955-06-07	PRIOR FILING DATE: 193-10-10-10-10-10-10-10-10-10-10-10-10-10-	. Facedith Vet. 2.7 1334 NA	### 1334 1.08e-205 Length: 1334	Oy 1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeuLeuVal 20

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